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OM protein - protein search, using sw model

Run on: January 12, 2004, 09:59:06 ; Search time 41 Seconds

(without alignments)  
30.971 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 561297

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	16	69.6	17	ABB07407	xyna fragment in p
2	16	69.6	20	AA178408	Human papillomavir
3	16	69.6	20	ABB07406	xyna fragment in p
4	16	69.6	32	AA138243	Human secreted pro
5	16	69.6	31	AA144053	Mutant hcs peptide
6	15	65.2	10	AAG94992	Human complementar
7	15	65.2	10	AAG94994	Human complementar
8	15	65.2	13	AAW86105	Peptide from human
9	15	65.2	13	AAW86092	Peptide from human

10	15	65.2	13	20	AAW86100	Peptide from human
11	15	65.2	15	23	ABG68859	CDR2 sequence remo
12	15	65.2	18	17	AAW89962	Synthetic human er
13	15	65.2	19	19	AAW70915	Peptide PEP2L, hom
14	15	65.2	19	22	ABG53230	Human liver peptid
15	15	65.2	19	22	ABB38408	Peptide #5914 enco
16	15	65.2	19	22	ABB23586	Protein #5585 enco
17	15	65.2	19	22	AAW59018	Human brain expres
18	15	65.2	19	22	AAW71548	Human bone marrow
19	15	65.2	19	22	AAW19201	Peptide #5635 enco
20	15	65.2	19	22	AAW1846	Peptide #5883 enco
21	15	65.2	19	23	ABG41359	Human peptide enco
22	15	65.2	20	19	AAW21167	Human bcl2 proto-o
23	15	65.2	20	20	AAW12576	Human 5' EST secre
24	15	65.2	20	22	AAW76893	Human colon cancer
25	15	65.2	21	19	AAW62904	Cytotoxic myristyl
26	15	65.2	24	20	AAW13017	Human secreted pro
27	15	65.2	27	21	AAW09354	Hepatitis GB virus
28	15	65.2	27	22	AAW61645	Tyrosinase peptide
29	15	65.2	28	19	AAW48994	Lipidated vaccine
30	15	65.2	28	19	AAW48994	Lipidated vaccine
31	15	65.2	28	20	AAW09328	Lipidated vaccine
32	15	65.2	28	20	AAW09329	Lipidated vaccine
33	15	65.2	28	21	AAW12420	HCW lipidated vac
34	15	65.2	28	21	AAW12421	HCW lipidated vac
35	15	65.2	28	22	AAW05439	Human cytomagalovi
36	15	65.2	28	22	AAW05440	Human cytomagalovi
37	15	65.2	28	23	AAW10852	Human cytomagalovi
38	15	65.2	28	23	AAW10853	Human cytomagalovi
39	15	65.2	30	23	AAW84889	Human Tyros segmen
40	15	65.2	31	21	AAW39014	Human secreted pep
41	15	65.2	32	22	ABG57579	Human liver peptid
42	15	65.2	32	22	ABW42148	Peptide #9654 enco
43	15	65.2	32	22	ABB25710	Protein #7709 enco
44	15	65.2	32	22	AAW63033	Human brain expres
45	15	65.2	32	22	AAW75844	Human bone marrow

#### ALIGNMENTS

RESULT 1  
ABB07407  
ID ABB07407 standard; Protein; 17 AA.  
AC ABB07407;  
XX  
DT 09-APR-2002 (first entry)  
XX  
xyna fragment in plasmid pXLIN2.1.  
DE  
Xylanase; xyna; transcriptional regulation; xylan; xylose; enzyme;  
KW fungal; pharmaceutical; food; chemical.  
XX  
OS Aureobasidium pullulans.  
XX  
FN WO200196578-A2.  
XX  
PD 20-DEC-2001.  
XX  
PF 14-JUN-2001; 2001WO-US19340.  
XX  
PR 15-JUN-2000; 2000US-0595344.  
XX  
PA (UWGB-) UNIV GEORGIA RES FOUND INC.  
XX  
PI Li X, Ljungdahl LG;  
XX  
DR WPI; 2002-130735/17.  
DR N-PSDB; ABA94594.  
XX  
PT New isolated nucleic acid encoding a signal peptide for efficient and economical secreted expression of a protein of interest in a eukaryotic

PT cell, widely used in pharmaceutical, food and chemical industries -

PS Example 2; Page 29; 43pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a

CC xylanase (xynA) transcriptional regulatory sequence operably linked to a

CC heterologous coding sequence. Provided is a method for producing a

CC heterologous protein in *Aureobasidium pullulans*, by up-regulating the

CC expression of a sequence encoding a heterologous protein by adding xylan

CC or xylose to a medium in which a recombinant *A. pullulans* cell comprising

CC the new isolated nucleic acid molecule is cultured, where the medium

CC contains glucose at a concentration less than 0.02 % (weight/volume) and

CC a xynA transcription regulatory sequence is operably linked to the

CC sequence encoding the heterologous protein, and the heterologous protein

CC is expressed. The nucleic acid containing a signal peptide-encoding

CC sequence, is useful for efficient and economical secreted expression of a

CC protein of interest in a eukaryotic cell, especially a fungal cell such

CC as *Aureobasidium pullulans*. It may be used as a probe. The proteins

CC produced are widely used in pharmaceutical, food, chemical and other

CC industries. The present sequence represents the xynA sequence around the

CC multiple cloning sites in plasmid pXLIN2.1.

XX

XX SQ Sequence 17 AA;

Query Match 69.6%; Score 16; DB 23; Length 17;

Best Local Similarity 25.0%; Pred. No. 3e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 4 WSSAAALG 11

RESULT 2

ID AAY78408 standard; peptide; 20 AA.

AC AAY78408;

DT 08-MAY-2000 (first entry)

XX

DE Human papillomavirus E7 protein inhibiting peptide SEQ ID NO:34.

XX

XX HPV; E7 protein; inhibition; virucide; carcinoma.

XX Human papillomavirus.

OS Synthetic.

XX

PN EP969013-A1.

XX

PD 05-JAN-2000.

XX

PF 30-JUN-1998; 98EP-0112047.

XX

PR 30-JUN-1998; 98EP-0112047.

XX

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA

PI Jansen-Duerr P, Zwerschke W;

XX

XX WPI; 2000-149116/14.

DR

XX

XX New peptides used for the prevention and treatment of human papilloma

PT virus associated disease -

PT

XX

PS Claim 1; Page 23; 26pp; English.

XX AAY78375 to AAY78415 represent peptides capable of inhibiting the human

CC papillomavirus (HPV) E7 protein. The peptides have virucide activity.

CC The peptides can be used in pharmaceutical compositions to inhibit

CC HPV E7 protein, which allows the prevention and/or treatment of HPV

CC associated diseases, which may comprise carcinomas.

XX

SQ Sequence 20 AA;

Query Match 69.6%; Score 16; DB 21; Length 20;

Best Local Similarity 25.0%; Pred. No. 3.5e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 5 WFSASAG 12

RESULT 3

ID ABB07406 standard; Protein; 20 AA.

AC ABB07406;

XX

DT 09-APR-2002 (first entry)

XX

DE xynA fragment in plasmid pXL2.1.

XX

XX xylanase; xynA; transcriptional regulation; xylan; xylose; enzyme;

KW fungal; pharmaceutical; food; chemical.

XX

OS *Aureobasidium pullulans*.

XX

PN WO200196578-A2.

XX

PD 20-DEC-2001.

XX

PF 14-JUN-2001; 2001WO-US19340.

XX

PR 15-JUN-2000; 2000US-0595344.

XX

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX

PI Li X, Ljungdahl LG;

DR

DR WPI; 2002-130735/17.

DR N-PSDB; ABA94593.

XX New isolated nucleic acid encoding a signal peptide for efficient and

PT economical secreted expression of a protein of interest in a eukaryotic

PT cell, widely used in pharmaceutical, food and chemical industries -

XX

PS Example 2; Page 29; 43pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a

CC xylanase (xynA) transcriptional regulatory sequence operably linked to a

CC heterologous coding sequence. Provided is a method for producing a

CC heterologous protein in *Aureobasidium pullulans*, by up-regulating the

CC expression of a sequence encoding a heterologous protein by adding xylan

CC or xylose to a medium in which a recombinant *A. pullulans* cell comprising

CC the new isolated nucleic acid molecule is cultured, where the medium

CC contains glucose at a concentration less than 0.02 % (weight/volume) and

CC a xynA transcription regulatory sequence is operably linked to the

CC sequence encoding the heterologous protein, and the heterologous protein

CC is expressed. The nucleic acid containing a signal peptide-encoding

CC sequence, is useful for efficient and economical secreted expression of a

CC protein of interest in a eukaryotic cell, especially a fungal cell such

CC as *Aureobasidium pullulans*. It may be used as a probe. The proteins

CC produced are widely used in pharmaceutical, food, chemical and other

CC industries. The present sequence represents the xynA sequence around the

CC multiple cloning sites in plasmid pXL2.1.

SQ Sequence 20 AA;

Query Match 69.6%; Score 16; DB 23; Length 20;

Best Local Similarity 25.0%; Pred. No. 3.5e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 7 WSSAAALG 14

RESULT 4  
ID AAB38243 standard; Protein; 32 AA.  
XX AAB38243;  
AC AAB38243;  
DT 30-JAN-2001 (first entry)  
XX Human secreted protein sequence encoded by gene 41 SEQ ID NO:99.  
DE Human, secreted protein; diagnosis; immunosuppressive; antiarthritic;  
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
KW cerebroprotective; neuroprotective; antibacterial; virucide;  
KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;  
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
KW wound healing; skin aging; food additive; preservative.  
XX Homo sapiens.  
OS WO200058469-A1.  
XX PN 05-OCT-2000.  
PD 23-MAR-2000; 2000WO-US07579.  
XX PF 26-MAR-1999; 9SUS-0126509.  
PR 07-JAN-2000; 2000US-0174853.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Rosen CA, Ruben SM, Komatsoulis G;  
XX WPI, 2000-594642/56.  
DR N-PSDB; AAC69495.  
XX Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
PT Claim 11; Page 375; 416pp; English.  
XX The polynucleotide sequences given in AAC69455 to AAC69502 encode the  
CC human secreted proteins given in AAB38203 to AAB38250. AAB38251 to  
CC AAB38320 represent human secreted polypeptide sequences and proteins  
CC homologous to them, which are given in the exemplification of the present  
CC invention. Human secreted proteins have activities based on the tissues  
CC and cells the genes are expressed in. Example of activities include:  
CC immunosuppressive; antiarthritic; antirheumatic; antiproliferative;  
CC cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;  
CC neuroprotective; antibacterial; virucide; fungicide; and  
CC ophthalmological. The polynucleotides and polypeptides can be used to  
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
CC in diagnosing a pathological condition or susceptibility to a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases, hyperproliferative disorders, cardiovascular  
CC disorders, cerebrovascular disorders, angiogenesis, nervous system  
CC disorders, infections caused by bacteria, viruses and fungi and ocular  
CC disorders. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities. AAC69446 to AAC69454 and  
CC AAB38202 represent sequences used in the exemplification of the present  
CC invention.  
XX SQ Sequence 32 AA;  
Query Match 69.6%; Score 16; DB 21; Length 32;

Best Local Similarity 25.0%; Pred. No. 5.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 10 WVSATATG 17

RESULT 5  
ID AAW44053 standard; peptide; 33 AA.  
XX AAW44053;  
AC AAW44053;  
DT 26-JUN-1998 (first entry)  
XX Mutant hCS peptide.  
DE Corticostatin; somatostatin; hCS peptide; hormone-producing tumour;  
KW gastric ulcer; dementia; growth disorder; hormone secretion regulation;  
KW digestive system regulation; neural inhibitor; therapy.  
XX Synthetic.  
OS WO9746668-A1.  
XX PN 11-DEC-1997.  
PD 05-JUN-1997; 97WO-JP01911.  
XX PF 15-OCT-1996; 96JP-0272422.  
PR 07-JUN-1996; 96JP-0146052.  
XX PR 19-SEP-1996; 96JP-0247710.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX PA Fukusumi S, Hinuma S, Kitada C;  
XX WPI, 1998-042177/04.  
DR N-PSDB; AAV02093.  
XX Peptide having corticostatin or somatostatin activity - useful as  
PT anticancer and antitumor agent, and for control of dementia and  
PT growth abnormalities  
PT Disclosure; Page 117; 174pp; Japanese.  
XX This sequence is a mutant hCS peptide. It is a peptide of the  
CC invention, and has corticostatin or somatostatin activity. Antibodies  
CC recognising hCS-17 can be used to screen for a compound that modulates,  
CC i.e. an agonist or antagonist, the binding of hCS-17 to its receptor, and  
CC to assay for hCS-17, e.g. diagnosis. hCS-17, the DNA encoding it or a  
CC receptor agonist or antagonist can be used to treat and prevent  
CC hormone-producing tumours (e.g. tumours producing gastrin or insulin),  
CC gastric ulcers and dementia, regulate sleep and control growth disorders  
CC (e.g. acromegaly, gigantism and dwarfism). They can also be used to  
CC regulate hormone secretion and the digestive system (e.g. to treat  
CC diabetes), and as tumour multiplication or neural inhibitors.  
XX SQ Sequence 33 AA;  
Query Match 69.6%; Score 16; DB 19; Length 33;  
Best Local Similarity 25.0%; Pred. No. 5.2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 13 WTSQASAG 20

RESULT 6  
ID AAG94992 standard; Peptide; 10 AA.  
ID AAG94992





CC given species; and (c) modifying the amino acid sequence to eliminate at  
 CC least one of the T-cell epitopes identified in step (b) thereby to  
 CC eliminate or reduce the immunogenicity of the protein when exposed to the  
 CC immune system of the given species. A method of analysing a pre-existing  
 CC protein to predict the basis for immunogenic responses is also provided.  
 CC The methods can be used particularly for reducing the immunogenicity of  
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase. The  
 CC products can be used for diagnosis and therapy. Sequences AAW86075-W86114  
 CC represent peptides from humanised A33 heavy chain variable region  
 CC predicted by peptide threading.

XX Sequence 13 AA;

Query Match 65.2%; Score 15; DB 20; Length 13;  
 Best Local Similarity 25.0%; Pred. No. 4.1e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
 DB 5 WVATISSG 12

#### RESULT 9

AAW86092  
 ID AAW86092 standard; peptide; 13 AA.

XX AAW86092;

DT 03-MAR-1999 (first entry)

DE Peptide from humanised A33 heavy chain variable region.

KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system;  
 immunoglobulin; therapeutic; streptokinase; diagnosis; human; A33.

XX Homo sapiens.

FN WO9852976-A1.

XX 26-NOV-1998.

PP 21-MAY-1998; 98WO-GB01473.

PR 14-APR-1998; 98GB-0007751.

PR 21-MAY-1997; 97GB-0010480.

PR 31-JUL-1997; 97GB-0016197.

PR 28-NOV-1997; 97GB-0025270.

PR 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FU;

XX WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid  
 PT sequence of the protein to eliminate potential epitopes for T-cells  
 PT of a given species

XX Example 5; Page 33; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic  
 CC proteins. The method comprises determining at least part of the amino  
 CC acid sequence of the protein; (b) identifying in the amino acid sequence  
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the  
 CC given species; and (c) modifying the amino acid sequence to eliminate at  
 CC least one of the T-cell epitopes identified in step (b) thereby to  
 CC eliminate or reduce the immunogenicity of the protein when exposed to the  
 CC immune system of the given species. A method of analysing a pre-existing  
 CC protein to predict the basis for immunogenic responses is also provided.  
 CC The methods can be used particularly for reducing the immunogenicity of  
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase. The  
 CC products can be used for diagnosis and therapy. Sequences AAW86075-W86114

CC represent peptides from humanised A33 heavy chain variable region  
 CC predicted by peptide threading.

XX Sequence 13 AA;

Query Match 65.2%; Score 15; DB 20; Length 13;  
 Best Local Similarity 25.0%; Pred. No. 4.1e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
 DB 2 WVATISSG 9

#### RESULT 10

AAW86100  
 ID AAW86100 standard; peptide; 13 AA.

XX AAW86100;

DT 03-MAR-1999 (first entry)

DE Peptide from humanised A33 heavy chain variable region.

KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system;  
 immunoglobulin; therapeutic; streptokinase; diagnosis; human; A33.

XX Homo sapiens.

FN WO9852976-A1.

XX 26-NOV-1998.

PP 21-MAY-1998; 98WO-GB01473.

PR 14-APR-1998; 98GB-0007751.

PR 21-MAY-1997; 97GB-0010480.

PR 31-JUL-1997; 97GB-0016197.

PR 28-NOV-1997; 97GB-0025270.

PR 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FU;

XX WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid  
 PT sequence of the protein to eliminate potential epitopes for T-cells  
 PT of a given species

XX Example 5; Page 34; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic  
 CC proteins. The method comprises determining at least part of the amino  
 CC acid sequence of the protein; (b) identifying in the amino acid sequence  
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the  
 CC given species; and (c) modifying the amino acid sequence to eliminate at  
 CC least one of the T-cell epitopes identified in step (b) thereby to  
 CC eliminate or reduce the immunogenicity of the protein when exposed to the  
 CC immune system of the given species. A method of analysing a pre-existing  
 CC protein to predict the basis for immunogenic responses is also provided.  
 CC The methods can be used particularly for reducing the immunogenicity of  
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase. The  
 CC products can be used for diagnosis and therapy. Sequences AAW86075-W86114  
 CC represent peptides from humanised A33 heavy chain variable region  
 CC predicted by peptide threading.

XX Sequence 13 AA;

Query Match 65.2%; Score 15; DB 20; Length 13;  
 Best Local Similarity 25.0%; Pred. No. 4.1e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
 DB 2 WWTATSSG 9

RESULT 11  
 ABG68859  
 ID ABG68859 standard; Peptide; 15 AA.  
 XX AC  
 XX ABG68859;  
 DT 07-OCT-2002 (first entry)  
 DE CDR2 sequence removed from cIFN $\gamma$  construct.  
 XX  
 KW Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective;  
 KW immunosuppressive; antiarthritic; cytokine receptor; interferon; IFN;  
 KW cancer; haematological malignancy; viral infection; hepatitis; human;  
 KW multiple sclerosis; autoimmune disease; arthritis.  
 XX  
 OS Synthetic.  
 XX WO200244197-A2.  
 PN 06-JUN-2002.  
 XX  
 PD 30-NOV-2001; 2001WO-CA01701.  
 PF 01-DEC-2000; 2000US-0727388.  
 PR (FISH/) FISH E N.  
 PA Fish EN;  
 XX WPI; 2002-547689/58.  
 DR N-PSDB; ABK97822.  
 XX  
 XX Cytokine receptor binding peptide construct, in particular interferon  
 PT receptor binding peptide construct for use as an interferon mimetic,  
 PT comprises a cytokine receptor binding domain incorporated in a  
 PT molecular scaffold -  
 XX  
 PS Example 8; Page 51; 105pp; English.

CC This invention relates to a novel cytokine receptor binding peptide  
 CC construct comprising a cytokine receptor binding domain incorporated in  
 CC a suitable molecular scaffold so that the scaffold maintains the binding  
 CC domain in a configuration suitable for binding to the cytokine receptor.  
 CC The peptides of the invention may have cytostatic, virucide,  
 CC hepatotropic, antiinflammatory, neuroprotective, immunosuppressive and  
 CC antiarthritic activities. A new interferon receptor binding peptide  
 CC construct is useful in the manufacture of a medicament as an interferon  
 CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in  
 CC medical therapies for cancer, haematological malignancies, viral  
 CC infections (hepatitis B or C), multiple sclerosis and autoimmune  
 CC diseases such as arthritis, to detect modulators of IFN action, in  
 CC screening assays to compare the activity and/or interaction with  
 CC another molecule or potential IFN modulator and also in the diagnosis  
 CC of IFN activity related disorders. A nucleic acid encoding the  
 CC peptide of the invention or is useful for the treatment and therapy of  
 CC the mentioned medical conditions. The peptide of the invention has less  
 CC side effect than those of native cytokines. The present sequence  
 CC represents an interferon receptor binding peptide of the invention.

XX  
 SQ Sequence 15 AA;  
 Query Match 65.2%; Score 15; DB 23; Length 15;  
 Best Local Similarity 25.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
 DB 2 WWTATSSG 9

RESULT 12  
 AAR89962  
 ID AAR89962 standard; peptide; 18 AA.  
 XX AC  
 XX AAR89962;  
 DT 28-SEP-1996 (first entry)  
 DE Synthetic human erythropoietin receptor peptide, SE-2B.  
 XX  
 KW Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;  
 KW erythropoiesis; erythrocyte production; epitope mapping.  
 XX  
 OS Synthetic.  
 XX WO9603438-A1.  
 PN 08-FEB-1996.  
 PD 26-JUL-1995; 95WO-US09458.  
 PF 26-JUL-1994; 94US-0280864.  
 PR (AMGE-) AMGEN INC.  
 PA Elliott SG;  
 PI WPI; 1996-117004/12.  
 DR  
 XX Monoclonal antibodies stimulating an erythropoietin receptor -  
 PT useful in diagnosis and treatment of patients having disorders  
 PT associated with low red blood cell levels, e.g. anaemia  
 XX  
 PS Example 6; Page 34; 61pp; English.

CC AAR89960-R89965 and AAR89936-R89939 are overlapping, synthetic human  
 CC erythropoietin receptor (shuEPOR) peptides which span residues 1 to  
 CC 244 of the human EPOR. The peptides are used to map the EPOR binding  
 CC epitope of an EPOR monoclonal antibody which binds to EPORs and  
 CC stimulates erythropoiesis by stimulating the proliferation and/or  
 CC differentiation of erythroid progenitor cells to erythrocytes.  
 CC Pharmaceutical compans. contg. the antibody may be used in the  
 CC diagnosis and treatment of patients having disorders associated with  
 CC low red blood cell levels, e.g. anaemia. The antibodies are also  
 CC useful in methods and kits for detecting EPORs in biological in  
 CC biological samples.

XX  
 SQ Sequence 18 AA;  
 Query Match 65.2%; Score 15; DB 17; Length 18;  
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
 DB 3 WEERASAG 10

RESULT 13  
 AAW70915  
 ID AAW70915 standard; peptide; 19 AA.  
 XX AC  
 XX AAW70915;  
 DT 14-OCT-1998 (first entry)  
 DE Peptide PEP2L, homologous to light chain CDR2 of antibody RS-348.  
 KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
 KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;

KW viral infection; inhibit; fusion; protection; transcription; translation;  
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.  
 XX Synthetic.  
 OS Mus sp.  
 XX PR2758331-A1.  
 PN 17-JUL-1998.  
 PD 14-JAN-1997; 97FR-0000300.  
 XX 14-JAN-1997; 97FR-0000300.  
 XX (UYBO-) UNIV BOURGOGNE.  
 PA Bourgeois C, Kohli E, Pothier P;  
 PI WPI; 1998-390320/34.  
 DR New peptide(s) recognising viral epitope with tropism to mucosa -  
 XX useful for, e.g. diagnosing, preventing and treating viral  
 PT infection(s)  
 PT Claim 8; Fig 5; 5lpp; French.  
 PS AAW70905-46 represent peptide sequences that can recognise, by  
 XX antigen-antibody type reactions, at least 1 epitope of a pathogenic  
 CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are  
 CC analogous to CDR regions of monoclonal antibodies specific for  
 CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR  
 CC regions of monoclonal antibodies specific for site III or IV of the  
 CC VP6 protein of rota virus (RV). The peptides can neutralise viral  
 CC infections and may also inhibit fusion between infected and uninfected  
 CC cells or cells and viruses. They provide passive or active protection  
 CC and/or inhibit transcription of the virus, so are useful as antiviral  
 CC agents or for prophylaxis, in human or veterinary medicine. The peptides  
 CC can be labelled and used to diagnose infection or contamination by the  
 CC virus. The peptides are particularly directed against RSV or RS but may  
 CC also be used against papilloma, adeno, entero, polio, influenza or  
 CC immune deficiency viruses.  
 XX SQ Sequence 19 AA;  
 Query Match 65.2%; Score 15; DB 19; Length 19;  
 Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 WXXXXXXG 8  
 Db 7 WASTRDSG 14  
 RESULT 14  
 ABG53230  
 ID ABG53230 standard; Peptide; 19 AA.  
 XX AC ABG53230;  
 XX 25-FEB-2003 (first entry)  
 DT Human liver peptide, SEQ ID No 31878.  
 DE Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 KW hypercholesterolaemia; coronary heart disease.  
 KW Homo sapiens.  
 OS WO200157273-A2.  
 XX 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US00664.  
 XX PF

XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488898/53.  
 DR Human genome-derived single exon nucleic acid probes useful for  
 XX analysing gene expression in human adult liver -  
 PT Claim 27; SEQ ID No 31878; 659pp; English.  
 PS The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult  
 CC liver. (I) may be used for predicting, measuring and displaying gene  
 CC expression in samples derived from human adult liver. The genes  
 CC identified may be involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which  
 CC is associated with coronary heart disease. ABG47348-ABG59930 represent  
 CC human liver single exon encoded peptides of the invention.  
 CC Note: The sequence information for this patent does not appear in the  
 CC printed specification but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 19 AA;  
 Query Match 65.2%; Score 15; DB 22; Length 19;  
 Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 WXXXXXXG 8  
 Db 3 WGRSSTTG 10  
 RESULT 15  
 ABB38408  
 ID ABB38408 standard; Peptide; 19 AA.  
 XX AC ABB38408;  
 XX 04-FEB-2002 (first entry)  
 DT Peptide #5914 encoded by human foetal liver single exon probe.  
 DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
 KW Homo sapiens.  
 OS WO200157277-A2.  
 XX 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US00669.  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 PR

XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2001-483447/52.  
 XX PT Human genome-derived single exon nucleic acid probes useful for  
 XX PT analyzing gene expression in human fetal liver -  
 XX PS Claim 27; SEQ ID NO 31043; 639pp. + sequence listing; English.  
 XX CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 19 AA;  
 Query Match 65.2%; Score 15; DB 22; Length 19;  
 Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 Db 3 WRRSSTTG 10

Search completed: January 12, 2004, 10:05:04  
 Job time : 42 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:11:07 ; Search time 70 seconds  
(without alignments)  
23.030 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 226452

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	69.6	50	11	US-09-948-783-125
2	15	65.2	10	11	US-09-572-404B-1186
3	15	65.2	10	11	US-09-572-404B-1186
4	15	65.2	13	12	US-10-300-215-60
5	15	65.2	13	12	US-10-300-215-68
6	15	65.2	13	12	US-10-300-215-73
7	15	65.2	18	12	US-10-364-276-6
8	15	65.2	19	9	US-09-864-761-38884
9	15	65.2	20	12	US-10-280-066-61
10	15	65.2	20	12	US-10-280-066-61
11	15	65.2	20	15	US-10-106-698-7667
12	15	65.2	22	12	US-10-307-724-127
13	15	65.2	22	12	US-10-307-724-129
14	15	65.2	27	8	US-08-424-550B-481
15	15	65.2	28	12	US-10-405-231-35

16	15	65.2	28	12	US-10-405-231-36
17	15	65.2	28	15	US-10-238-607-35
18	15	65.2	28	15	US-10-238-607-36
19	15	65.2	31	12	US-09-962-756-1276
20	15	65.2	31	12	US-10-253-471-1276
21	15	65.2	32	9	US-09-864-761-41008
22	15	65.2	34	11	US-09-764-891-4811
23	15	65.2	34	15	US-10-091-572-366
24	15	65.2	36	11	US-09-883-343A-69
25	15	65.2	36	12	US-09-962-756-1310
26	15	65.2	36	12	US-10-253-471-1310
27	15	65.2	37	9	US-09-864-761-40556
28	15	65.2	37	15	US-10-007-521-64
29	15	65.2	39	9	US-09-864-761-48977
30	15	65.2	39	12	US-10-029-386-33891
31	15	65.2	40	12	US-10-029-386-33430
32	15	65.2	43	12	US-09-880-573-57
33	15	65.2	44	9	US-09-864-761-34910
34	15	65.2	44	9	US-09-864-761-37541
35	15	65.2	44	9	US-09-864-761-40294
36	15	65.2	44	9	US-09-864-761-44325
37	15	65.2	46	15	US-10-106-698-7164
38	15	65.2	46	15	US-10-106-698-7164
39	15	65.2	47	10	US-09-764-877-1793
40	15	65.2	49	9	US-09-864-761-41134
41	15	65.2	50	9	US-09-864-761-46317
42	14	60.9	8	10	US-09-185-908-163
43	14	60.9	9	10	US-09-185-908-163
44	14	60.9	9	10	US-09-835-948-72
45	14	60.9	9	12	US-10-172-597-72

#### ALIGNMENTS

RESULT 1  
US-09-948-783-125  
; Sequence 125, Application US/09948783  
; Publication No. US20030100051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: P2028P2  
; CURRENT APPLICATION NUMBER: US/09/948,783  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,846  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: 09/892,877  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 09/437,658  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/09847  
; PRIOR FILING DATE: 1999-05-06  
; PRIOR APPLICATION NUMBER: 60/085,093  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,094  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,105  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,180  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,927  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,906  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,924  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18

Sequence 36, Appl  
Sequence 35, Appl  
Sequence 36, Appl  
Sequence 1276, Ap  
Sequence 1276, Ap  
Sequence 41008, A  
Sequence 4811, Ap  
Sequence 366, Appl  
Sequence 69, Appl  
Sequence 1310, Ap  
Sequence 1310, Ap  
Sequence 40556, A  
Sequence 64, Appl  
Sequence 48977, A  
Sequence 33891, A  
Sequence 32430, A  
Sequence 57, Appl  
Sequence 34910, A  
Sequence 37541, A  
Sequence 40294, A  
Sequence 44325, A  
Sequence 7164, Ap  
Sequence 7164, Ap  
Sequence 1793, Ap  
Sequence 41134, A  
Sequence 46317, A  
Sequence 42, Appl  
Sequence 163, Appl  
Sequence 72, Appl  
Sequence 72, Appl

Mon Jan 12 08:42:31 2004

PRIOR APPLICATION NUMBER: 60/085,925  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,928  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,920  
PRIOR FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 465  
SOFTWARE: Patentin ver. 2.0  
SEQ ID NO 125  
LENGTH: 50  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-948-783-125

Query Match 69.6%; Score 15; DB 11; Length 50;  
Best Local Similarity 25.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 34 WTSSMATG 41

RESULT 2  
US-09-572-404B-1186  
Sequence 1186, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 1186  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in TMPO at 231-240 and may interact with Sequenc  
US-09-572-404B-1186

Query Match 65.2%; Score 15; DB 11; Length 10;  
Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 2 WTSGSSKG 9

RESULT 3  
US-09-572-404B-1188  
Sequence 1188, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 1188  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in TMPO at 230-239 and may interact with Sequenc  
US-09-572-404B-1188

Query Match 65.2%; Score 15; DB 11; Length 10;  
Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 2 WTSGSSKG 9

RESULT 4  
US-10-300-215-60  
Sequence 60, Application US/10300215  
Publication No. US20030153043A1  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
APPLICANT: ADAIR, Fiona Suzanne  
APPLICANT: HAMILTON, Anita Anne  
APPLICANT: CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
FILE REFERENCE: MER-104-Con.1  
CURRENT APPLICATION NUMBER: US/10/300,215  
CURRENT FILING DATE: 2002-11-20  
PRIOR APPLICATION NUMBER: US 09/438,136  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
PRIOR FILING DATE: 1998-05-21  
PRIOR APPLICATION NUMBER: GB 9710480.6  
PRIOR FILING DATE: 1997-05-21  
PRIOR APPLICATION NUMBER: GB 9716197.0  
PRIOR FILING DATE: 1997-07-31  
PRIOR APPLICATION NUMBER: GB 9725270.4  
PRIOR FILING DATE: 1997-11-28  
PRIOR APPLICATION NUMBER: GB 9807751.4  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/067,235  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 254  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 60  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: humanized monoclonal antibody fragments  
US-10-300-215-60

Query Match 65.2%; Score 15; DB 12; Length 13;  
Best Local Similarity 25.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 2 WVATISSG 9

RESULT 5  
US-10-300-215-68  
Sequence 68, Application US/10300215  
Publication No. US20030153043A1  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
APPLICANT: ADAIR, Fiona Suzanne  
APPLICANT: HAMILTON, Anita Anne  
APPLICANT: CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
FILE REFERENCE: MER-104-Con.1  
CURRENT APPLICATION NUMBER: US/10/300,215  
CURRENT FILING DATE: 2002-11-20  
PRIOR APPLICATION NUMBER: US 09/438,136  
PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: 60/085,925  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,928  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,920  
PRIOR FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 465  
SOFTWARE: Patentin ver. 2.0  
SEQ ID NO 125  
LENGTH: 50  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-948-783-125

Query Match 69.6%; Score 15; DB 11; Length 50;  
Best Local Similarity 25.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 34 WTSSMATG 41

RESULT 2  
US-09-572-404B-1186  
Sequence 1186, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 1186  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in TMPO at 231-240 and may interact with Sequenc  
US-09-572-404B-1186

Query Match 65.2%; Score 15; DB 11; Length 10;  
Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 2 WTSGSSKG 9

RESULT 3  
US-09-572-404B-1188  
Sequence 1188, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 1188  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in TMPO at 230-239 and may interact with Sequenc  
US-09-572-404B-1188

Query Match 65.2%; Score 15; DB 11; Length 10;  
Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 2 WTSGSSKG 9

RESULT 4  
US-10-300-215-60  
Sequence 60, Application US/10300215  
Publication No. US20030153043A1  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
APPLICANT: ADAIR, Fiona Suzanne  
APPLICANT: HAMILTON, Anita Anne  
APPLICANT: CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
FILE REFERENCE: MER-104-Con.1  
CURRENT APPLICATION NUMBER: US/10/300,215  
CURRENT FILING DATE: 2002-11-20  
PRIOR APPLICATION NUMBER: US 09/438,136  
PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
PRIOR FILING DATE: 1998-05-21  
PRIOR APPLICATION NUMBER: GB 9710480.6  
PRIOR FILING DATE: 1997-05-21  
PRIOR APPLICATION NUMBER: GB 9716197.0  
PRIOR FILING DATE: 1997-07-31  
PRIOR APPLICATION NUMBER: GB 9725270.4  
PRIOR FILING DATE: 1997-11-28  
PRIOR APPLICATION NUMBER: GB 9807751.4  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/067,235  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 254  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 68  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: humanized monoclonal antibody fragments  
US-10-300-215-68

Query Match 65.2%; Score 15; DB 12; Length 13;  
Best Local Similarity 25.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 2 WVATISSG 9

RESULT 6  
US-10-300-215-73  
Sequence 73, Application US/10300215  
Publication No. US20030153043A1  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
APPLICANT: ADAIR, Fiona Suzanne  
APPLICANT: HAMILTON, Anita Anne  
APPLICANT: CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
FILE REFERENCE: MER-104-Con.1  
CURRENT APPLICATION NUMBER: US/10/300,215  
CURRENT FILING DATE: 2002-11-20  
PRIOR APPLICATION NUMBER: US 09/438,136  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
PRIOR FILING DATE: 1998-05-21  
PRIOR APPLICATION NUMBER: GB 9710480.6  
PRIOR FILING DATE: 1997-05-21  
PRIOR APPLICATION NUMBER: GB 9716197.0  
PRIOR FILING DATE: 1997-07-31  
PRIOR APPLICATION NUMBER: GB 9725270.4  
PRIOR FILING DATE: 1997-11-28  
PRIOR APPLICATION NUMBER: GB 9807751.4  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/067,235  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 254  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 73  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: humanized monoclonal antibody fragments  
US-10-300-215-73

Query Match 65.2%; Score 15; DB 12; Length 13;  
Best Local Similarity 25.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 5 WVATISSG 12

RESULT 7  
US-10-364-276-6  
Sequence 6, Application US/10364276  
Publication No. US20030215444A1  
GENERAL INFORMATION:  
APPLICANT: Elliott, Steven G  
TITLE OF INVENTION: Antibodies which Activate an Erythropoietin Receptor  
FILE REFERENCE: 06843-0030-04000  
CURRENT APPLICATION NUMBER: US/10/364,276  
CURRENT FILING DATE: 2003-06-17  
PRIOR APPLICATION NUMBER: 09/092,671  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 08/280,864  
PRIOR FILING DATE: 1994-07-26  
PRIOR APPLICATION NUMBER: 09/640,090  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-364-276-6

Query Match 65.2%; Score 15; DB 12; Length 18;  
Best Local Similarity 25.0%; Pred. No. 8e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 3 WEEAASAG 10

RESULT 8  
US-09-864-761-38884  
Sequence 38884, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeonica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30

Mon Jan 12 08:42:31 2004

PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
SEQ ID NO 38884  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC004624.6  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
US-09-864-761-38884

Query Match 65.2%; Score 15; DB 9; Length 19;  
Best Local Similarity 25.0%; Pred. No. 8.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 3 WKRSSTTG 10

RESULT 9  
US-10-280-066-61  
Sequence 61, Application US/10280066  
Publication No. US20030180718A1  
GENERAL INFORMATION:  
APPLICANT: Pillutla, Renuka C.  
APPLICANT: Brissette, Renee  
APPLICANT: Spruyt, Michael  
APPLICANT: Dedova, Olga  
APPLICANT: Blume, Arthur J.  
APPLICANT: Prendergast, John  
APPLICANT: Goldstein, Neil I.  
TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND  
FILE REFERENCE: 2598-4009US1  
CURRENT APPLICATION NUMBER: US/10/280,066  
CURRENT FILING DATE: 2002-10-24  
PRIOR APPLICATION NUMBER: 60/345,471  
PRIOR FILING DATE: 2001-10-24  
NUMBER OF SEQ ID NOS: 537  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 61  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: MISC FEATURE  
OTHER INFORMATION: DGI-2-20F-PP-E7  
US-10-280-066-61

Query Match 65.2%; Score 15; DB 12; Length 20;  
Best Local Similarity 25.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 10 WTASRTGG 17

RESULT 10  
US-10-280-066-94  
Sequence 94, Application US/10280066  
Publication No. US20030180718A1  
GENERAL INFORMATION:  
APPLICANT: Pillutla, Renuka C.  
APPLICANT: Brissette, Renee  
APPLICANT: Spruyt, Michael  
APPLICANT: Dedova, Olga  
APPLICANT: Blume, Arthur J.  
APPLICANT: Prendergast, John  
APPLICANT: Goldstein, Neil I.  
TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BI  
FILE REFERENCE: 2598-4009US1  
CURRENT APPLICATION NUMBER: US/10/280,066  
CURRENT FILING DATE: 2002-10-24  
PRIOR APPLICATION NUMBER: 60/345,471  
PRIOR FILING DATE: 2001-10-24  
NUMBER OF SEQ ID NOS: 537  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 94  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: MISC FEATURE  
OTHER INFORMATION: DGI-2-20R-3-D9  
US-10-280-066-94

Query Match 65.2%; Score 15; DB 12; Length 20;  
Best Local Similarity 25.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 8 WASGSGAG 15

RESULT 11  
US-10-106-698-7667  
Sequence 7667, Application US/10106698  
Publication No. US20030109690A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept  
FILE REFERENCE: PA005PI  
CURRENT APPLICATION NUMBER: US/10/106,698  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: PCT/US00/26524  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/157,137  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: US 60/163,280  
PRIOR FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 8564  
SOFTWARE: PatentIn Ver. 3.0  
SEQ ID NO 7667  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (16)  
US-10-106-698-7667



OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: MISC FEATURE  
LOCATION: (19)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-7667

Query Match 65.2%; Score 15; DB 15; Length 20;  
Best Local Similarity 25.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 4 WAAQSSG 11

## RESULT 12

US-10-307-724-127  
Sequence 127, Application US/10307724  
Publication No. US20030232972A1  
GENERAL INFORMATION:  
APPLICANT: Bowdish, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Renshaw, Mark  
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
FILE REFERENCE: 1087-2c1p  
CURRENT APPLICATION NUMBER: US/10/307,724  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: US 60/251,448  
PRIOR FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: US 60/288,889  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 60/294,068  
PRIOR FILING DATE: 2001-05-29  
PRIOR APPLICATION NUMBER: US 10/006,593  
PRIOR FILING DATE: 2001-12-05  
NUMBER OF SEQ ID NOS: 134  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 127  
LENGTH: 22  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: heavy chain CDR2 clone  
US-10-307-724-127

Query Match 65.2%; Score 15; DB 12; Length 22;  
Best Local Similarity 25.0%; Pred. No. 9.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 14 WLAARAAG 21

## RESULT 13

US-10-307-724-129  
Sequence 129, Application US/10307724  
Publication No. US20030232972A1  
GENERAL INFORMATION:  
APPLICANT: Bowdish, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Renshaw, Mark  
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
FILE REFERENCE: 1087-2c1p  
CURRENT APPLICATION NUMBER: US/10/307,724  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: US 60/251,448  
PRIOR FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: US 60/288,889  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 60/294,068  
PRIOR FILING DATE: 2001-05-29  
PRIOR APPLICATION NUMBER: US 10/006,593

PRIOR FILING DATE: 2001-12-05  
NUMBER OF SEQ ID NOS: 134  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 129  
LENGTH: 22  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: heavy chain CDR2 clone  
US-10-307-724-129

Query Match 65.2%; Score 15; DB 12; Length 22;  
Best Local Similarity 25.0%; Pred. No. 9.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 14 WLAARATG 21

## RESULT 14

US-08-424-550B-481  
Sequence 481, Application US/08424550B  
Publication No. US20020119447A1  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUERHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550B  
FILING DATE:

CLASSIFICATION: 435435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 481:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-481

Query Match 65.2%; Score 15; DB 8; Length 27;  
Best Local Similarity 25.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY1 WXXXXXXG 8

DB14 WTRSSALG 21

RESULT 15

US-10-405-231-35

Sequence 35, Application US/10405231

Publication No. US20030190328A1

GENERAL INFORMATION:

APPLICANT: Diamond, Don J.

TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS

FILE REFERENCE: 1954-346

CURRENT APPLICATION NUMBER: US/10/405,231

CURRENT FILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: US/09/692,170C

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: US 09/534,639

PRIOR FILING DATE: 2000-03-27

PRIOR APPLICATION NUMBER: US 09/075,257

PRIOR FILING DATE: 1998-05-11

PRIOR APPLICATION NUMBER: US 09/021,298

PRIOR FILING DATE: 1998-02-10

PRIOR APPLICATION NUMBER: US 08/950,064

PRIOR FILING DATE: 1997-10-14

PRIOR APPLICATION NUMBER: US 08/747,488

PRIOR FILING DATE: 1996-11-12

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 35

LENGTH: 28

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic construct for human cytomegalovirus vaccine

FEATURE:

NAME/KEY: LIPID

LOCATION: (1)..(1)

OTHER INFORMATION: DIPALMITATE

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (6)..(6)

OTHER INFORMATION: Xaa = F or cyclohexylalanine

US-10-405-231-35

Query Match 65.2%; Score 15; DB 12; Length 28;

Best Local Similarity 25.0%; Pred. No. 1.1e+04;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY1 WXXXXXXG 8

DB10 WTLKAAAG 17

Search completed: January 12, 2004, 08:21:32

Job time : 73 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 12, 2004, 08:08:00 ; Search time 37 Seconds  
(without alignments)  
20.793 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 11832

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	65.2	41	2	hemoglobin AI - tu
2	15	65.2	43	2	hypothetical prote
3	14	60.9	9	2	delta sleep-induci
4	14	60.9	11	2	T-cell receptor ga
5	14	60.9	11	2	T-cell receptor ga
6	14	60.9	20	2	T-cell receptor be
7	14	60.9	27	2	AP24 protein - tom
8	14	60.9	27	2	amylase / pullulan
9	14	60.9	34	2	cellulase (BC 3.2.
10	14	60.9	37	2	osmotin I - common
11	14	60.9	37	2	thaumatin homolog
12	14	60.9	40	2	photosystem II cen
13	14	60.9	40	2	photosystem II pro
14	14	60.9	41	2	hemoglobin BIII -
15	14	60.9	50	2	hypothetical prote
16	14	60.9	50	2	probable cold stre
17	13	56.5	18	2	DNA topoisomerase
18	13	56.5	19	2	T-cell receptor ga
19	13	56.5	21	2	major outer membra
20	13	56.5	21	2	carbonic anhydrase
21	13	56.5	21	2	osmotin homolog -
22	13	56.5	22	2	fimbrial adhesin C
23	13	56.5	22	2	virg 6 protein - Bo
24	13	56.5	23	2	alkaline trypsin-1
25	13	56.5	23	2	virB protein - Agr
26	13	56.5	26	2	phospholipase A2 (
27	13	56.5	26	2	phospholipase A2 (
28	13	56.5	28	2	phospholipase A2 (
29	13	56.5	28	2	phospholipase A2 (

30 13 56.5 30 2 S68639  
31 13 56.5 30 2 S68640  
32 13 56.5 30 2 H97596  
33 13 56.5 31 2 S31075  
34 13 56.5 34 2 S68880  
35 13 56.5 35 2 H84214  
36 13 56.5 35 2 D85762  
37 13 56.5 36 2 A81740  
38 13 56.5 37 2 S71912  
39 13 56.5 37 2 PC1121  
40 13 56.5 37 2 S54441  
41 13 56.5 38 2 A39558  
42 13 56.5 38 2 S40096  
43 13 56.5 39 2 S01813  
44 13 56.5 39 2 S71913  
45 13 56.5 39 2 S73309

nigroxin A - black  
nigroxin B - black  
hypothetical prote  
hypothetical prote  
ribulose-bisphosph  
hypothetical prote  
probable outer mem  
hemoglobin, extrac  
anti-fungal 25K pro  
hypothetical prote  
phospholipase A2 (

## ALIGNMENTS

## RESULT 1

S01807

hemoglobin AI - tube worm (Lamellibrachia sp.) (fragment)

C;Species: Lamellibrachia sp.

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 04-Mar-2000

C;Accession: S01807

R;Suzuki, T.; Takagi, T.; Ohta, S.

Biochem. J. 255, 541-545, 1988

A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkab

A;Reference number: S01807; PMID:89076216; PMID:3202832

A;Accession: S01807

A;Molecule type: protein

A;Residues: 1-41 &lt;SUZ&gt;

C;Superfamily: globin; globin homology

C;Keywords: oxygen carrier

Query Match 65.2%; Score 15; DB 2; Length 41;

Best Local Similarity 25.0%; Pred. No. 1.6e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8

Db 15 WASVYSSG 22

## RESULT 2

A97416

hypothetical protein AGR\_C\_830 [imported] - Agrobacterium tumefaciens (strain C58, Ceri

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002

C;Accession: A97416

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldma

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu

A;Reference number: A97359; PMID:21608551; PMID:11743194

A;Accession: A97416

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-43 &lt;KUR&gt;

A;Cross-references: GB:AE007869; PIDN:AAK86282.1; PID:G15155394; GSPDB:GN00169

A;Gene: AGR\_C\_830

A;Map position: circular chromosome

Query Match

Best Local Similarity 65.2%; Score 15; DB 2; Length 43;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8

Db 20 WTWTKSAG 27

Mon Jan 12 08:42:31 2004

### RESULT 3

ODRB

delta sleep-inducing peptide - rabbit  
C:/Species/Oryctolagus cuniculus (domestic rabbit)  
C:/Date/20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
Accession No. A01422  
R;Name/Species M.; Dudley L.; Gachter, R.; Maier, P.F.; Tobler, H.J.; Schoenenberger, G.A.  
Experimental 3; 548-552, 1977  
Affiliation The delta sleep inducing peptide (DSIP). Comparative properties of the original  
Affiliations number. A01422. PMID: 77185324. MSID: 862769

A;Reference number: A01422; MOLECULAR WEIGHT: 1422  
A;Accession: A01422  
A;Molecule type: protein  
A;Residues: 1-9 <MON>  
C;Comment: This peptide was obtained from dialyates of occipital venous sinus blood from recipient rabbits, it induces spindle and delta EEG activity and reduced motor activity of C.Superfamily: unassigned animal peptides

Query Match	60.9%	Score 14;	DB 2;	Length 9;
Best Local Similarity	25.0%	Pred. No. 2.8e+05;		
Mismatches	0;	Mismatches	6;	Indels
Conservative	0;	Conservative	0;	Gaps

Qy	1	WXXXXXXG	8
Dh	1	WAGGDASG	8

#### RESULT 4:

C38887  
T-cell receptor gamma chain (Sa.3)' - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C/Accession: C38887  
R/Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A>Title: Rearrangement and functional site sequence analyses of T-cell receptor gamma gene  
A/Accession: A41946. MIMD:92049316. PMID:16558619

A/Accession: C38887  
A/Reference number: A115740; NCBI:25135216; EMBL:AF010316; GenBank:AF010316; not compared with conceptual translation  
A/Accession: C38887  
A/Reference number: A115740; NCBI:25135216; EMBL:AF010316; GenBank:AF010316; not compared with conceptual translation

```
A;Status: preliminary;  
A;Molecule type: DNA  
A;Residues: 1-11 <WHE>
```

Query Match 60.9%; Score 14; DB 2; Length 11;  
 Best Local Similarity 25.0%; Pred. No. 1.2e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
3 WAGRDSSG 10

RESIST 5

A14946  
 T-cell receptor gamma chain (St.1) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
 C:Accession: I41946  
 R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
 Mol. Cell. Biol. 11, 5902-5909, 1991  
 A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma 9  
 A:Reference number: A1946; MUID:92049316; PMID:1658619  
 A:Accession: I41946  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-11 <WHE>  
 C:Keywords: T-cell receptor

Query Match	60.9%;	Score 14;	DB 2;	Length 11;
Best Local Similarity	25.0%;	Pred. No. 1.2e+03;		
Matches	3;	Conservative	0;	Mismatches 6;
				Indels 0;
				Gaps 0;

Qy 1 WXXXXXXXXX 8  
nb 3 WAGGPDSSG 10

## RESULT. 6

F49048 T-cell receptor beta chain v region (CDR3 junction, clone Vbeta20.1) - human (fragment).  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C:Accession: F49048  
R:Stoud, M.; Kjeidsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.  
Eur. J. Immunol. 22, 2413-2418, 1992  
A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juveni.  
b:Reference number: F49048; MUID: 92387250; PMID:1387614

A:Accession: F49048  
A:Accession: F49048  
A:Status: preliminary; not compared with conceptual translation  
A:Title: IL-2R $\alpha$  amino acid sequence  
A:Molecule type: mRNA  
A:Residues: 1-20 <SIO>  
A:Experimental source: patient SS, IL-2R $\alpha$  synovial T-cells  
A:Note: sequence extracted from NCBI backbone (NCBIP113268)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 60.9%; Score 14; DB 2; Length 20;  
Best Local Similarity 25.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Caps 0;

Qy 1 WXXXXXXG 8  
9 WSATGVYG 16

## RESULT 7

A:Accession: PQ0170  
 A:Title: Pathogen-induced proteins with inhibitory activity toward Phytophthora infestans  
 A:Reference number: PQ0169; PMID:1841721  
 A:Accession: PQ0170  
 A:Molecule type: protein  
 A:Residues: 1-27 <WOL>  
 A:Experimental source: cv. Moneymaker  
 C:Comment: This protein causes lysis of sporangia and growth inhibition of Phytophthora  
 C:Superfamily: thaumatin I  
 C:Accession: PQ0170  
 C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 28-Apr-1995  
 C:Species: Lycopersicon esculentum (tomato)  
 A:24 protein - tomato (fragment)  
 A:24 protein - tomato (fragment)  
 R:Woloshek, C.P.; Meutenhoff, J.S.; Sela-Buurlage, M.; van den Elzen, P.J.M.; Cornelis

Query Match 60.9%; Score 14; DB 2; Length 27;  
Best Local Similarity 25.0%;  
Pred. No. 2.4e+03;  
Matches 0; Mismatches 6; Indels 2; Conservative

Qy 1 WXXXXXXG 8  
|  
14 WAASTPIG 21  
nb

## RESULT 8

S69372 amy1ase / pullulanase - Bacillus circulans (fragment)  
 C/Species: Bacillus circulans  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
 C/Accession: S69372  
 R:Kim, C.H.; Kim, Y.S.  
 Eur. J. Biochem. 227, 687-693, 1995  
 A/Title: Substrate specificity and detailed characterization of a bifunctional  
 A/Accession number: S69372 MIMD:95172052 PMID:7532585

A:Accession: S69372  
A:Molecule type: protein  
A:Residues: 1-27 <IM>  
A: is inconsistent with that from abstract in having 23

Query Match 60.9%; Score 14; DB 2; Length 27;  
 Best Local Similarity 25.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 Db 15 WAAGIVTG 22

RESULT 9  
 S13662  
 Cellulase (EC 3.2.1.4) - fungus (Sclerotinia sclerotiorum) (fragment)  
 N;Alternate names: endo-1,4-beta-glucanase  
 C;Species: Sclerotinia sclerotiorum  
 C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
 C;Accession: S13662  
 R;Waksman, G.  
 Biochim. Biophys. Acta 1073, 49-55, 1991  
 A;Title: Purification and characterization of two endo-beta-1,4-D-glucanases from Sclerotinia sclerotiorum  
 A;Reference number: S13662; PMID:91120823; PMID:1991146  
 A;Accession: S13662  
 A;Molecule type: protein  
 A;Residues: 1-34 <BIO>  
 A;Experimental source: strain de Bary  
 C;Function:  
 A;Pathway: cellulose degradation  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 60.9%; Score 14; DB 2; Length 34;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 Db 8 WIGASEG 15

RESULT 10  
 D44957  
 osmotin I - common tobacco (cv. Samsun NN) (fragment)  
 C;Species: Nicotiana tabacum (common tobacco)  
 C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 12-Apr-1995  
 C;Accession: D44957  
 R;Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.  
 Plant Cell Physiol. 31, 215-221, 1990  
 A;Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum  
 A;Reference number: A44957  
 A;Accession: D44957  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-37 <TAK>  
 C;Superfamily: thaumatin I

Query Match 60.9%; Score 14; DB 2; Length 37;  
 Best Local Similarity 25.0%; Pred. No. 3e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 Db 14 WAASTPIG 21

RESULT 11  
 S17684  
 thaumatin homolog 2 - barley  
 C;Species: Hordeum vulgare (barley)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
 C;Accession: S17684  
 R;Hejgaard, J.; Jacobsen, S.; Svendsen, I.  
 FEBS Lett. 291, 127-131, 1991  
 A;Title: Two antifungal thaumatin-like proteins from barley grain.  
 A;Reference number: S17573; PMID:92037994; PMID:1936240

Query Match 60.9%; Score 14; DB 2; Length 37;  
 Best Local Similarity 25.0%; Pred. No. 3e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 Db 14 WAAAVPAG 21

RESULT 12  
 T06869  
 photosystem II center protein psbJ - Cyanophora paradoxa cyanelle  
 C;Species: cyanelle Cyanophora paradoxa  
 C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 26-Aug-1999  
 C;Accession: T06869  
 R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.  
 submitted to the EMBL Data Library, July 1995  
 A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.  
 A;Reference number: Z15840  
 A;Accession: T06869  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-40 <STI>  
 A;Cross-references: EMBL:U30821; NID:G1016083; PIDN:AAA81212.1; PID:G1016125  
 A;Experimental source: strain Pringsheim LB555  
 C;Genetics:  
 A;Genome: cyanelle  
 A;Note: psbJ  
 C;Superfamily: photosystem II protein psbJ  
 C;Keywords: cyanelle; photosynthesis; photosystem II; thylakoid

Query Match 60.9%; Score 14; DB 2; Length 40;  
 Best Local Similarity 25.0%; Pred. No. 3.1e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 Db 11 WLVAIVAG 18

RESULT 13  
 AI2286  
 photosystem II protein J [imported] - Nostoc sp. (strain PCC 7120)  
 C;Species: Nostoc sp. PCC 7120  
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C;Accession: AI2286  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriugu  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
 DNA Res. 8, 205-213, 2001  
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A  
 A;Reference number: AB1807; PMID:11759840  
 A;Accession: AI2286  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-40 <KUR>  
 A;Cross-references: GB:BA000019; PIDN:BA075547.1; PID:G17132982; GSPDB:GN00179  
 A;Experimental source: strain PCC 7120  
 C;Genetics:  
 A;Gene: psbJ  
 C;Superfamily: photosystem II protein psbJ

Query Match 60.9%; Score 14; DB 2; Length 40;  
 Best Local Similarity 25.0%; Pred. No. 3.1e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8

Mon Jan 12 08:42:31 2004

us-09-185-908-1.slim50.rpr

Job time : 40 secs

Db 11 WWTATAG 18

RESULT 14

S01815 hemoglobin BIII - tube worm (Lamellibrachia sp.) (fragment)

C:Species: Lamellibrachia sp.

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 04-Mar-2000

C:Accession: S01815

R:Suzuki, T.; Takagi, T.; Ohta, S.

Biochem. J. 255, 541-545, 1988

A:Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably

A:Reference number: S01807; PMID:3202832

A:Accession: S01815

A:Molecule type: protein

A:Residues: 1-41 <SUZ>

C:Superfamily: globin; globin homology

C:Keywords: oxygen carrier

Query Match 60.9%; Score 14; DB 2; Length 41;

Best Local Similarity 25.0%; Pred. No. 3.2e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8

Db 15 WAEYGSQ 22

RESULT 15

F82719 hypothetical protein XF1135 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: F82719

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A8515; PMID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: F82719

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-50 <SIM>

A:Cross-references: GB:AE003849; GB:AE003849; NID:g9106088; PIDN:AAF83945.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F

as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, B.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1135

Query Match 60.9%; Score 14; DB 2; Length 50;

Best Local Similarity 25.0%; Pred. No. 3.7e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8

Db 41 WEALFASG 48

Search completed: January 12, 2004, 08:11:02

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2004, 08:07:57 ; Search time 24 Seconds  
(without alignments)  
15.676 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 4018

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	15	65.2	34	1 MYTA MYTED
2	15	65.2	41	1 GLB1_LAMSP
3	14	60.9	9	1 DMS5 PHYSA
4	14	60.9	29	1 DMS5 PHYSA
5	14	60.9	33	1 RUGA_RANRU
6	14	60.9	34	1 GUNI_SCLSC
7	14	60.9	35	1 NEP_FVLIH3
8	14	60.9	37	1 THRS_HORVU
9	14	60.9	39	1 PSBJ_SYN7
10	14	60.9	40	1 PSBJ_ANASP
11	14	60.9	40	1 PSBJ_CVAPA
12	14	60.9	40	1 PSBJ_GINBI
13	14	60.9	40	1 PSBJ_SYNEL
14	13	56.5	17	1 NEP_FVLIJ3
15	13	56.5	18	1 TOP1_KLEAE
16	13	56.5	24	1 PCL1_PACGO
17	13	56.5	24	1 PCL2_PACGO
18	13	56.5	26	1 PCW3_PACGO
19	13	56.5	28	1 PA22_MICNI
20	13	56.5	28	1 PA23_MICNI
21	13	56.5	29	1 TLP_ACTDE
22	13	56.5	37	1 PIFL_ACHLY
23	13	56.5	38	1 PA21_MATBI
24	13	56.5	39	1 MCP1_SOLTU
25	13	56.5	39	1 PSBJ_GUITH
26	13	56.5	39	1 PSBJ_FORPU
27	13	56.5	39	1 PSBJ_SYN2
28	13	56.5	40	1 PSBJ_ARATH
29	13	56.5	40	1 PSBJ_HORVU
30	13	56.5	40	1 PSBJ_LOTUA
31	13	56.5	40	1 PSBJ_MAGTA
32	13	56.5	40	1 PSBJ_MAIZE
33	13	56.5	40	1 PSBJ_MARPO

34	13	56.5	40	1 PSBJ_ORNHO	Q9mrk7 oenothera h
35	13	56.5	40	1 PSBJ_ORYSA	P12189 oryza sativ
36	13	56.5	40	1 PSBJ_PEA	P13555 pisum sativ
37	13	56.5	40	1 PSBJ_PINTH	P41618 pinus thum
38	13	56.5	40	1 PSBJ_POPDE	P92417 populus del
39	13	56.5	40	1 PSBJ_PSIUO	Q8wi06 psilotum nu
40	13	56.5	40	1 PSBJ_SECCO	P19053 secale cere
41	13	56.5	40	1 PSBJ_SPIOL	Q9mj12 spinacia ol
42	13	56.5	40	1 PSBJ_TOBAC	P12190 nicotiana t
43	13	56.5	42	1 PSBJ_CVAPA	P19153 cyanophora
44	13	56.5	42	1 PSBJ_CHAGL	Q8msx0 chaetophae
45	13	56.5	42	1 PSBJ_CHLVU	P56338 chlorella v

## ALIGNMENTS

RESULT 1				
MYTA MYTED	STANDARD;	PRT;	34 AA.	
AC P81612;				
DT 30-MAY-2000 (Rel. 39, Created)				
DT 30-MAY-2000 (Rel. 39, Last sequence update)				
DT 15-SEP-2003 (Rel. 42, Last annotation update)				
DE Mytilin A.				
OS Mytilus edulis (Blue mussel).				
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;				
OC Mytiloidea; Mytilidae; Mytilus.				
OX NCBI_TaxID=6550;				
RN [1]				
RP SEQUENCE, AND CHARACTERIZATION.				
RC TISSUE=Blood.				
RX MEDLINE=96355569; PubMed=8702979;				
RA Charlet M., Chernysh S., Philippe H., Hetru C., Hoffman J.A.,				
RA Bulet P.;				
RT "Innate immunity. Isolation of several cysteine-rich antimicrobial				
RT peptides from the blood of a mollusc, Mytilus edulis.";				
RL J. Biol. Chem. 271:21808-21813(1996).				
CC - FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST A.VIRIDANS,				
CC B.MEGATERIUM, M.LUTEUS, E.FAECALIS, S.AUREUS AND E.COLI.				
CC IT IS ACTIVE AGAINST THE MARINE SPECIES A.CARRAGEENOVORA,				
CC P.ALGINOVORA AND C.DROBACHENSIS.				
CC -!- PTM: THE CYSTEINE RESIDUES PRESUMABLY EXIST IN INTRAMOLECULAR				
CC DISULFIDE BRIDGES.				
CC -!- MASS SPECTROMETRY: MW=3773.7; METHOD=MALDI.				
KW Antibiotic.				
SQ SEQUENCE 34 AA; 3781 MW; F61805D5500CA698 CRC64;				
Query Match 65.2%; Score 15; DB 1; Length 34;				
Best Local Similarity 25.0%; Pred. No. 6.2e+02;				
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY 1 WXXXXXXG 8				
Db 18 WASASFRG 25				
RESULT 2				
GLB1_LAMSP	STANDARD;	PRT;	41 AA.	
ID GLB1_LAMSP				
AC P20412;				
DT 01-FEB-1991 (Rel. 17, Created)				
DT 01-FEB-1991 (Rel. 17, Last sequence update)				
DT 28-FEB-2003 (Rel. 41, Last annotation update)				
DE Giant hemoglobin AI chain (Fragment).				
OS Lamellibrachia sp. (Deep-sea giant tube worm).				
OC Eukaryota; Metazoa; Pogonophora; Vestimentifera; Basibranchia;				
OC Lamellibrachia; Lamellibrachidae; Lamellibrachia.				
OX NCBI_TaxID=6424;				
RN [1]				
RP SEQUENCE.				
RX MEDLINE=89076216; PubMed=3202832;				
RA Suzuki T., Takagi T., Ohta S.;				

RT "N-terminal amino acid sequence of the deep-sea tube worm haemoglobin  
RT remarkably resembles that of annelid haemoglobin.";  
RL Biochem J. 255:541-545(1988).

CC -1- SUBUNIT: GIANT HEMOGLOBIN IS COMPOSED OF FOUR HEME-CONTAINING  
CC CHAINS (AI TO AIV), AND TWO LINKER CHAINS (AV AND AVI).

CC -1- SIMILARITY: Belongs to the globin family.

CC PIR: S01807; S01807.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; Globin; 1.

DR PROSITE: PS01033; GLOBIN; PARTIAL.

KW Heme; Oxygen transport; Transport.

FT NON TER 41

SQ SEQUENCE 41 AA; 4572 MW; 673E6629936FA5D9 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 41;

Best Local Similarity 25.0%; Pred. No. 7.2e+02;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 15 WASVYSSG 22

## RESULT 3

ID\_DSIP\_RABIT STANDARD; PRT; 9 AA.

AC P01158;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Delta sleep-inducing peptide (DSIP).

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RN SEQUENCE.

RX MEDLINE=77185324; PubMed=862769;

RA Monnier M., Dudley L., Gachter R., Maier P.F., Tobler H.J.,

RA Schoenenberger G.A.,

RA "The delta sleep inducing peptide (DSIP). Comparative properties of

RT the original and synthetic nonapeptide.";

RL Experientia 33:548-552(1977).

RN [2]

RN SEQUENCE, AND SYNTHESIS.

RX MEDLINE=79054421; PubMed=568769;

RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.,

RA "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid

RT analysis, sequence, synthesis and activity of the nonapeptide.";

RL Pflugers Arch. 376:119-129(1978).

RN [3]

RN REVIEW.

RX MEDLINE=87175129; PubMed=3550726;

RA Graf M.V., Kastin A.J.,

RA "Delta-sleep-inducing peptide (DSIP): an update.";

RL Peptides 7:1165-1187(1986).

CC -1- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF

CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND

CC REDUCED MOTOR ACTIVITIES.

CC -1- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF

CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC

CC STIMULATION OF THE THALAMUS.

CC -1- DATABASE: NAME=Protein Spotlight;

CC NOTE=Issue 8 of March 2001;

CC WWW="http://www.expasy.org/spotlight/articles/spltt008.html".

CC PIR: A01422; QDRB.

DR PIR: A01422; QDRB.

SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;

Query Match 60.9%; Score 14; DB 1; Length 9;

Best Local Similarity 25.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

Db 1 WAGGDASG 8

## RESULT 4

DMS5\_PHYSA STANDARD; PRT; 29 AA.

AC P80281;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Dermaseptin 5 (DS V).

OS Phyllomedusa sauvagii (Savage's leaf frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Phyllomedusinae; Phyllomedusa.

OX NCBI\_TaxID=8395;

RN [1]

RN SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=94139686; PubMed=8306981;

RA Mor A., Nicolas P.,

RA "Isolation and structure of novel defensive peptides from frog skin.";

RL Eur. J. Biochem. 219:145-154(1994).

CC -1- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST

CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE

CC FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Skin.

CC -1- SIMILARITY: Belongs to the frog skin active peptide (PSAP) family.

CC Dermaseptin subfamily.

CC Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.

KW Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;

SQ SEQUENCE 29 AA; 2840 MW; 540A4971FC5BB506 CRC64;

Query Match 60.9%; Score 14; DB 1; Length 29;

Best Local Similarity 25.0%; Pred. No. 1.1e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 3 WSKIRTAG 10

## RESULT 5

RUGA\_RANRU STANDARD; PRT; 33 AA.

AC P80954;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Rugosin A.

OS Rana rugosa (Wrinkled frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.

OX NCBI\_TaxID=8410;

RN [1]

RN SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=95336450; PubMed=7612013;

RA Suzuki S., Ohe Y., Kagegawa T., Tatemoto K.,

RT "Isolation and characterization of novel antimicrobial peptides,

RL rugosins A, B and C, from the skin of the frog, Rana rugosa.";

RL Biochem. Biophys. Res. Commun. 212:249-254(1995).

CC -1- FUNCTION: Has antibacterial activity against Gram-positive

CC bacteria.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: SKIN.

CC -1- SIMILARITY: Belongs to the brevinin family.

KW Amphibian defense peptide; Antibiotic.

FT DISULFID 27 33

SQ SEQUENCE 33 AA; 3440 MW; E41DA4CF3916CA4C CRC64;

Query Match

60.9%; Score 14; DB 1; Length 33;



Best Local Similarity 25.0%; Pred. No. 1.2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 9 WAISAKG 16

RESULT 6  
GUNI\_SCLSC  
ID GUN1\_SCLSC STANDARD; PRT; 34 AA.  
AC P21833;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Endoglucanase 1 (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)  
DE (EG1) (Fragment).  
OS Sclerotinia sclerotiorum.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;  
OC Helotiales; Sclerotiniaceae; Sclerotinia.  
OX NCBI\_TaxID=5180;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=91120823; PubMed=1991146;  
RA Waksman G.;  
RT "Purification and characterization of two endo-beta-1,4-D-glucanases  
from Sclerotinia sclerotiorum";  
RL Biochim. Biophys. Acta 1073:49-55 (1991).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
linkages in cellulose, lichenin and cereal beta-D-glucans.  
CC -1- MISCELLANEOUS: ACTIVE TOWARDS CARBOXYMETHYL CELLULOSE AND  
4-METHYLBELLIFERYL CELLOBIOSIDE.  
CC -1- SIMILARITY: TO S. COMMUNE EGI.  
DR PIR; S13662; S13662.  
KW Cellulose degradation; Hydrolase; Glycosidase.  
FT NON\_TER 34 34  
SQ SEQUENCE 34 AA; 3452 MW; 9F83ACFF75FC9F78 CRC64;

Query Match 60.9%; Score 14; DB 1; Length 34;  
Best Local Similarity 25.0%; Pred. No. 1.2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 8 WICASESG 15

RESULT 7  
NEF\_HV1H3  
ID NEF\_HV1H3 STANDARD; PRT; 35 AA.  
AC P05854;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Negative factor (P-protein) (27 kDa protein) (3' ORF) (Fragment).  
GN NEF.  
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11707;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85228248; PubMed=2988795;  
RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,  
RA Shaw G.M., Wong-Staal F., Reddy E.P.;  
RT "HIV-III env gene products synthesized in E. coli are recognized by  
antibodies present in the sera of AIDS patients.";  
RL Cell 41:979-986 (1985).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling

an oncogene product".  
Nature 330:266-269 (1987).  
-1- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating  
activities. It seems to down-regulate the CD4(T4) antigen.  
-----  
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-----  
EMBL; M14100; AAA44680.1; --  
HIV; M14100; NEFSHXB3.  
InterPro; IPR001558; HIV\_Nef.  
Pfam; PF00469; F-protein; 1.  
ProDom; PD000031; HIV\_Nef; 1.  
KW AIDS; Myristate; GTP-Binding.  
FT LIPID 2 2 MYRISTATE.  
FT NON\_TER 35 35  
SQ SEQUENCE 35 AA; 3714 MW; F66354AFBE1DFCFE CRC64;

Query Match 60.9%; Score 14; DB 1; Length 35;  
Best Local Similarity 25.0%; Pred. No. 1.2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 5 WSKSSVWG 12

RESULT 8  
THHS\_HORVU  
ID THHS\_HORVU STANDARD; PRT; 37 AA.  
AC P33045;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Antifungal protein S (Fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=CV. BOMI RISO 1508;  
RX MEDLINE=92037994; PubMed=1936240;  
RA Heigaard J., Jacobsen S., Svendsen I.;  
RT "Two antifungal thaumatin-like proteins from barley grain.";  
RL FEBS Lett. 291:127-131 (1991).  
CC -1- FUNCTION: HAS ANTIFUNGAL ACTIVITY. INHIBITS THE GROWTH OF  
TRICHODERMA VIRIDAE AND CANDIDA ALBICANS.  
CC -1- SIMILARITY: Belongs to the thaumatin family.  
DR PIR; S17684; S17684.  
DR HSP; P33679; IDU5.  
DR InterPro; IPR001938; Thaumatin.  
DR Pfam; PF00314; thaumatin; 1.  
DR ProDom; PD001321; Thaumatin; 1.  
DR PROSITE; PS00316; THAUMATIN; PARTIAL.  
KW Plant defense; Fungicide.  
FT NON\_TER 37 37  
SQ SEQUENCE 37 AA; 3871 MW; 7BE164CCBE8A9881 CRC64;

Query Match 60.9%; Score 14; DB 1; Length 37;  
Best Local Similarity 25.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 14 WAAAVPAG 21

Mon Jan 12 08:42:32 2004

photosystem II; its exact function is not yet known.  
 -1- SIMILARITY: Belongs to the psbJ family.  
 -----  
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 -----  
 EMBL; AP003594; BAB75547.1; --  
 PIR; A12286; A12286.  
 HAMAP; MF 01305; -; 1.  
 InterPro; IPR002682; PSII\_PsbJ.  
 Pfam; PF01788; PsbJ; 1.  
 ProDom; PD003776; PSII\_PsbJ; 1.  
 Photosynthesis; Photosystem II; Reaction center; Transmembrane;  
 KW Complete proteome.  
 FT TRANSMEM 10 32 POTENTIAL.  
 SQ SEQUENCE 40 AA; 3973 MW; 2P6D7354C19A6303 CRC64;  
 Query Match 60.9%; Score 14; DB 1; Length 40;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 DB 11 WVATVAG 18  
 RESULT 11  
 PSBJ\_CYP4A STANDARD; PRT; 40 AA.  
 ID PSBJ\_CYP4A  
 AC P19155;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Photosystem II reaction center J protein.  
 GN PSBJ.  
 OS Cyanophora paradoxa.  
 OC Eukaryota.  
 OC Glaucomastophyceae; Cyanophoraceae; Cyanophora.  
 OX NCBI\_TaxID=2762;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UTEX LB 555 / Pringsheim;  
 RA Cantrell A., Bryant D.A.;  
 RT "Nucleotide sequence of the genes encoding cytochrome b-559 from the cyanelle genome of Cyanophora paradoxa."  
 RL Photosyn. Res. 16:65-81(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UTEX LB 555 / Pringsheim;  
 RA Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J., Bryant D.A.;  
 RT "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa."  
 RL Plant Mol. Biol. Rep. 13:327-332(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UTEX LB 555 / Pringsheim;  
 RA Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M., Farley J.Y., Schlachter W.M., Chung S., Newmann-Spallart C., Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;  
 RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa: the genetic complexity of a primitive plastid."  
 RL (in) Schenk H.B.A., Herrmann R., Jeon K.W., Mueller N.E., Schwemmler W. (eds.);  
 RL Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg (1997).  
 CC -1- FUNCTION: This protein is a component of the reaction center of photosystem II; its exact function is not yet known.  
 CC -1- SIMILARITY: Belongs to the psbJ family.

photosystem II; its exact function is not yet known.  
 -1- SIMILARITY: Belongs to the psbJ family.  
 -----  
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 -----  
 EMBL; AY120853; AM82677.1; --  
 HAMAP; MF 01305; -; 1.  
 InterPro; IPR002682; PSII\_PsbJ.  
 Pfam; PF01788; PsbJ; 1.  
 Photosynthesis; Photosystem II; Reaction center; Transmembrane.  
 KW TRANSMEM 7 29 POTENTIAL.  
 FT SEQUENCE 39 AA; 3842 MW; CE55851E75CD63F0 CRC64;  
 Query Match 60.9%; Score 14; DB 1; Length 39;  
 Best Local Similarity 25.0%; Pred. No. 1.3e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 DB 10 WIVATVAG 17  
 RESULT 10  
 PSBJ\_ANASP STANDARD; PRT; 40 AA.  
 ID PSBJ\_ANASP  
 AC Q8YQH9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Photosystem II reaction center J protein.  
 GN PSBJ OR ASR3848.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."  
 RL DNA Res. 8:205-213(2001).  
 CC -1- FUNCTION: This protein is a component of the reaction center of

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-----  
EMBL; M35129; AAA31698.1; --  
EMBL; U30821; AAA81212.1; --  
PIR; T06869; T06869.  
DR HAMAP; MF\_01305; --; 1.  
DR InterPro; IPR002682; PSII\_PsbJ.  
DR Pfam; PF01788; PsbJ; 1.  
KW Photosynthesis; Photosystem II; Reaction center; Cyanelle;  
KW Transmembrane.  
FT TRANSMEM 10 32 POTENTIAL.  
SQ SEQUENCE 40 AA; 3972 MW; A40746C06B44B5D8 CRC64;  
  
Query Match 60.9%; Score 14; DB 1; Length 40;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 11 WLVTAVAG 18  
  
RESULT 12  
PSBJ\_GINBI STANDARD; PRT; 40 AA.  
ID PSBJ\_GINBI  
AC Q9TH21;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Photosystem II reaction center J protein.  
GN PSBJ.  
OS Ginkgo biloba (Ginkgo).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.  
OX NCBI\_TaxID=3311;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99321801; PubMed=10393241;  
RA Kudla J., Bock R.;  
RT "RNA editing in an untranslated region of the Ginkgo chloroplast genome."  
RL Gene 234:81-86(1999).  
CC -!- FUNCTION: This protein is a component of the reaction center of photosystem II; its exact function is not yet known.  
CC -!- SIMILARITY: Belongs to the psbJ family.  
CC  
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EMBL; AJ130891; CAB61494.1; --  
EMBL; HAMAP; MF\_01305; --; 1.  
DR InterPro; IPR002682; PSII\_PsbJ.  
DR Pfam; PF01788; PsbJ; 1.  
DR ProDom; PD003776; PSII\_PsbJ; 1.  
KW Photosynthesis; Photosystem II; Reaction center; Chloroplast;  
KW Transmembrane.  
FT TRANSMEM 7 29 POTENTIAL.  
SQ SEQUENCE 40 AA; 4197 MW; 4ADC35F5B0F37A2 CRC64;  
  
Query Match 60.9%; Score 14; DB 1; Length 40;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 11 WLVTAVAG 18  
  
RESULT 13  
PSBJ\_SYNEL STANDARD; PRT; 40 AA.  
ID PSBJ\_SYNEL  
AC P59087;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Photosystem II reaction center J protein.  
GN PSBJ OR TSRI544.  
OS Synechococcus elongatus (Thermosynechococcus elongatus).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID=32046;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=BP-1;  
RX MEDLINE=22225144; PubMed=12240834;  
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1";  
RL DNA Res. 9:123-130(2002).  
CC -!- FUNCTION: This protein is a component of the reaction center of photosystem II; its exact function is not yet known.  
CC -!- SIMILARITY: Belongs to the psbJ family.  
CC  
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EMBL; AP005374; BAC09096.1; --  
EMBL; HAMAP; MF\_01305; --; 1.  
DR InterPro; IPR002682; PSII\_PsbJ.  
DR Pfam; PF01788; PsbJ; 1.  
DR ProDom; PD003776; PSII\_PsbJ; 1.  
KW Photosynthesis; Photosystem II; Reaction center; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 10 32 POTENTIAL.  
SQ SEQUENCE 40 AA; 4105 MW; 4D05FAA8C690069E CRC64;  
  
Query Match 60.9%; Score 14; DB 1; Length 40;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 11 WLVTAVAG 18  
  
RESULT 14  
NEF\_HVIJ3 STANDARD; PRT; 17 AA.  
ID NEF\_HVIJ3  
AC P12780;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3' ORF) (Fragment).  
GN NEF.  
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.

Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 11 WLVTAVAG 18  
  
RESULT 13  
PSBJ\_SYNEL STANDARD; PRT; 40 AA.  
ID PSBJ\_SYNEL  
AC P59087;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Photosystem II reaction center J protein.  
GN PSBJ OR TSRI544.  
OS Synechococcus elongatus (Thermosynechococcus elongatus).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID=32046;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=BP-1;  
RX MEDLINE=22225144; PubMed=12240834;  
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1";  
RL DNA Res. 9:123-130(2002).  
CC -!- FUNCTION: This protein is a component of the reaction center of photosystem II; its exact function is not yet known.  
CC -!- SIMILARITY: Belongs to the psbJ family.  
CC  
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EMBL; AP005374; BAC09096.1; --  
EMBL; HAMAP; MF\_01305; --; 1.  
DR InterPro; IPR002682; PSII\_PsbJ.  
DR Pfam; PF01788; PsbJ; 1.  
DR ProDom; PD003776; PSII\_PsbJ; 1.  
KW Photosynthesis; Photosystem II; Reaction center; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 10 32 POTENTIAL.  
SQ SEQUENCE 40 AA; 4105 MW; 4D05FAA8C690069E CRC64;  
  
Query Match 60.9%; Score 14; DB 1; Length 40;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 11 WLVTAVAG 18  
  
RESULT 14  
NEF\_HVIJ3 STANDARD; PRT; 17 AA.  
ID NEF\_HVIJ3  
AC P12780;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3' ORF) (Fragment).  
GN NEF.  
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.

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CC -----  
DR EMBL; X78729; -; NOT\_ANNOTATED\_CDS.  
DR HSP; P06612; IYUA.  
DR InterPro; IPR000380; DNA\_topoisomerase.  
DR PROSITE; PS00396; TOPOISOMERASE\_I\_PROK; PARTIAL.  
KW Isomerase; Topoisomerase; DNA-binding.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2043 MW; 8C1C81238F0BEFA4 CRC64;  
  
Query Match 56.5%; Score 13; DB 1; Length 18;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 4 WSAFFIDG 11

Search completed: January 12, 2004, 08:08:40  
Job time : 26 secs

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CC -----  
DR EMBL; M21138; AAB03527.1; -;  
DR HIV; M21138; NEPSJH3.  
DR InterPro; IPR001558; HIV\_Nef.  
DR Pfam; PF00469; P-protein; 1.  
KW AIDS; Myristate; GTP-binding.  
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1901 MW; 6B6B3F26FEB921E CRC64;  
  
Query Match 56.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 5 WSKRSVVG 12

RESULT 15  
TOP1\_KLEAE STANDARD; PRT; 18 AA.  
AC P46155;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)  
DE (Twisting enzyme) (Swivelase) (Fragment).  
GN TOPA.  
OS Klebsiella aerogenes.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=28451;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=NTC 418 / ATCC 15380;  
RX MEDLINE=94220019; PubMed=8166630;  
RA Lynch A.S.; Tyrrell R.; Smerdon S.J.; Briggs G.S.; Wilkinson A.J.;  
RT "Characterization of the CyeB protein of Klebsiella aerogenes: direct  
RT evidence that N-acetylserine rather than O-acetylserine serves as the  
RT inducer of the cysteine regulon."  
RL Biochem. J. 299:129-136(1994).  
CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE  
CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.  
CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded  
CC DNA, followed by passage and rejoining.  
CC -1- SUBUNIT: Monomer (By similarity).  
CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA  
CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN  
CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS  
CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.  
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC TYPE I/III TOPOISOMERASE  
CC FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2004, 08:08:01 ; Search time 82 Seconds  
(without alignments)  
25.176 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 39761

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	65.2	15	8	O99386 sus scrofa
2	15	65.2	27	4	Q8WUA6 homo sapien
3	15	65.2	27	12	Q9I41 hepatitis c
4	15	65.2	27	12	Q9I41 hepatitis c
5	15	65.2	27	12	Q9I31 hepatitis c
6	15	65.2	27	12	Q9I28 hepatitis c
7	15	65.2	27	12	Q9I15 hepatitis c
8	15	65.2	27	12	Q9I34 hepatitis c
9	15	65.2	27	12	Q9I46 hepatitis c
10	15	65.2	27	12	Q9I46 hepatitis c
11	15	65.2	27	12	Q9I23 hepatitis c
12	15	65.2	27	12	Q9I21 hepatitis c
13	15	65.2	27	12	Q9I27 hepatitis c
14	15	65.2	27	12	Q9I39 hepatitis c
15	15	65.2	27	12	Q9I18 hepatitis c
16	15	65.2	27	12	Q9I35 hepatitis c
					Q9I26 hepatitis c

17	15	65.2	27	12	Q9I37 hepatitis c
18	15	65.2	27	12	Q9I25 hepatitis c
19	15	65.2	27	12	Q9PX19 hepatitis c
20	15	65.2	27	12	Q9IIM1 hepatitis c
21	15	65.2	27	12	Q9I14 hepatitis c
22	15	65.2	27	12	Q9I20 hepatitis c
23	15	65.2	27	12	Q9I33 hepatitis c
24	15	65.2	27	12	Q9I36 hepatitis c
25	15	65.2	27	12	Q9I29 hepatitis c
26	15	65.2	27	12	Q9I45 hepatitis c
27	15	65.2	27	12	Q9I12 hepatitis c
28	15	65.2	27	12	Q9I13 hepatitis c
29	15	65.2	27	12	Q9I24 hepatitis c
30	15	65.2	27	12	Q9I38 hepatitis c
31	15	65.2	27	12	Q9I11 hepatitis c
32	15	65.2	27	12	Q9IIM0 hepatitis c
33	15	65.2	27	12	Q9I30 hepatitis c
34	15	65.2	27	12	Q9I22 hepatitis c
35	15	65.2	27	12	Q9IIM2 hepatitis c
36	15	65.2	27	12	Q9I42 hepatitis c
37	15	65.2	31	2	Q93GF8
38	15	65.2	35	4	Q94783
39	15	65.2	37	12	Q8J202
40	15	65.2	37	12	Q8J204
41	15	65.2	40	15	Q9QGF9
42	15	65.2	42	9	Q9T022
43	15	65.2	43	16	Q8U5K3
44	15	65.2	45	15	Q9QGF1
45	14	60.9	12	15	O41611

## ALIGNMENTS

## RESULT 1

O99386 ID O99386 PRELIMINARY; PRT; 15 AA.  
AC O99386;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DE 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
DE Cytochrome oxidase subunit 2 (Fragment).  
GN COII  
OS Sus scrofa (pig).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Periphera blood;  
RX MEDLINE=98403943; PubMed=9734874;  
RA Tartaglia M., Saulle E.;  
RT "Rapid communication: nucleotide sequence of porcine and ovine tRNA (lys) and ATPase8 mitochondrial genes.";  
RL J. Anim. Sci. 76:2207-2208(1998).  
DR EMBL; AF039170; AAD05063.1; -  
KW Mitochondrion.  
FT NON TER  
SQ SEQUENCE 15 AA; 1788 MW; 2B93E0B6A0588CB3 CRC64;

Query Match 65.2%; Score 15; DB 8; Length 15;  
Best Local Similarity 25.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 8 WSTSMITG 15

## RESULT 2

Q8WUA6 ID Q8WUA6 PRELIMINARY; PRT; 27 AA.

Mon Jan 12 08:42:32 2004

```

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Alberto S.-F.;
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the
RL histological outcome of liver transplantation.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221264; AAF77829.1; -.
DR InterPro; IPR002531; HCV NS1.
DR Pfam; PF01560; HCV NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2887 MW; D250829C29407A6D CRC64;

Query Match 65.2%; Score 15; DB 12; Length 27;
Best Local Similarity 25.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8
DB 15 WTLFSSG 22

RESULT 5
Q91J28 PRELIMINARY; PRT; 27 AA.
ID Q91J28
AC Q91J28;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope protein (Genome polyprotein) (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Alberto S.-F.;
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the
RL histological outcome of liver transplantation.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221267; AAF77829.1; -.
DR InterPro; IPR002531; HCV NS1.
DR Pfam; PF01560; HCV NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;

Query Match 65.2%; Score 15; DB 12; Length 27;
Best Local Similarity 25.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8
DB 15 WTLFSSG 22

RESULT 6
Q91J15 PRELIMINARY; PRT; 27 AA.
ID Q91J15
AC Q91J15;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope protein (Genome polyprotein) (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

```

OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasiespecies in the  
RT histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF221280; AAF77842.1; -;  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 27 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

RESULT 7  
Q9IJ34  
ID Q9IJ34 PRELIMINARY; PRT; 27 AA.  
AC Q9IJ34;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasiespecies in the  
RT histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF221261; AAF77823.1; -;  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 27 27  
SQ SEQUENCE 27 AA; 2797 MW; D250928159407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

RESULT 8  
Q9IJ44  
ID Q9IJ44 PRELIMINARY; PRT; 27 AA.  
AC Q9IJ44;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.

OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasiespecies in the  
RT histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF221251; AAF77813.1; -;  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 27 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

RESULT 9  
Q9IJ46  
ID Q9IJ46 PRELIMINARY; PRT; 27 AA.  
AC Q9IJ46;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasiespecies in the  
RT histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF221249; AAF77811.1; -;  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 27 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

RESULT 10  
Q9IJ23  
ID Q9IJ23 PRELIMINARY; PRT; 27 AA.  
AC Q9IJ23;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;

RP SEQUENCE FROM N.A.  
 RA Alberto S.-F.;  
 RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
 RL histological outcome of liver transplantation.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF221268; AAF77830.1; -  
 DR InterPro; IPR002531; HCV\_NSI.  
 DR Pfam; PF01560; HCV\_NSI; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 27  
 SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
 Query Match 65.2%; Score 15; DB 12; Length 27;  
 Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 Db 15 WTLFSSG 22

RESULT 13  
 Q9IUJ39 PRELIMINARY; PRT; 27 AA.  
 AC Q9IUJ39;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope protein (Genome polyprotein) (Fragment).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OC NCBI\_TaxID=11103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Alberto S.-F.;  
 RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
 RL histological outcome of liver transplantation.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF221268; AAF77830.1; -  
 DR InterPro; IPR002531; HCV\_NSI.  
 DR Pfam; PF01560; HCV\_NSI; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 27  
 SQ SEQUENCE 27 AA; 2811 MW; C95132805944A14D CRC64;  
 Query Match 65.2%; Score 15; DB 12; Length 27;  
 Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 Db 15 WTLFSSG 22

RESULT 14  
 Q9IUJ18 PRELIMINARY; PRT; 27 AA.  
 AC Q9IUJ18;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope protein (Genome polyprotein) (Fragment).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OC NCBI\_TaxID=11103;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.  
 RA Alberto S.-F.;  
 RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
 RL histological outcome of liver transplantation.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF221268; AAF77830.1; -  
 DR InterPro; IPR002531; HCV\_NSI.  
 DR Pfam; PF01560; HCV\_NSI; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 27  
 SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
 Query Match 65.2%; Score 15; DB 12; Length 27;  
 Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 Db 15 WTLFSSG 22

RESULT 11  
 Q9IUJ21 PRELIMINARY; PRT; 27 AA.  
 AC Q9IUJ21;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope protein (Genome polyprotein) (Fragment).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OC NCBI\_TaxID=11103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Alberto S.-F.;  
 RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
 RL histological outcome of liver transplantation.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF221268; AAF77830.1; -  
 DR InterPro; IPR002531; HCV\_NSI.  
 DR Pfam; PF01560; HCV\_NSI; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 27  
 SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
 Query Match 65.2%; Score 15; DB 12; Length 27;  
 Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 Db 15 WTLFSSG 22

RESULT 12  
 Q9IUJ27 PRELIMINARY; PRT; 27 AA.  
 AC Q9IUJ27;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope protein (Genome polyprotein) (Fragment).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OC NCBI\_TaxID=11103;  
 RN [1]  
 RP SEQUENCE FROM N.A.



RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF221277; AAF77839.1; -.  
DR InterPro; IPR002531; HCV\_NSI.  
DR Pfam; PF01560; HCV\_NSI; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;

Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

## RESULT 15

Q91J35 PRELIMINARY; PRT; 27 AA.  
AC Q91J35;  
DT 01-OCT-2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF221260; AAF77822.1; -.  
DR InterPro; IPR002531; HCV\_NSI.  
DR Pfam; PF01560; HCV\_NSI; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;

Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

Search completed: January 12, 2004, 08:13:23  
Job time : 86 secs

! FINDPATTERNS on geneseqp:\* allowing 0 mismatches

1 ! W(K,R)XX(S,A)(Y,F)XG January 12, 2004 10:24 ..  
AAR04585 ck: 2828 len: 513 ! Aar04585 Aquaricine I. 3/2003  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
495: AGYYL WRIYAYSG SGMYE  
AAR13181 ck: 2828 len: 513 ! Aar13181 T.aquaticus Aquaricin 1. 10/1991  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
495: AGYYL WRIYAYSG SGMYE  
AAR67653 ck: 2828 len: 513 ! Aar67653 Aqualysin I. 8/1995  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
495: AGYYL WRIYAYSG SGMYE  
AAR97244 ck: 1074 len: 4,473 ! Aar97244 Virulence gene cluster polypeptide  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
1,144: KALAN WKPAAPQG IPORL  
AAW82254 ck: 7849 len: 934 ! Aaw82254 JPl0248575 Seq ID 4. 7/1999  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
79: EDGTW WRSRAYHG KLGKY  
AAY41726 ck: 2066 len: 211 ! Aay41726 Human PRO944 protein sequence. 12/  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
30: TALPQ WRIYSYAG DNIVT  
AAY30337 ck: 9802 len: 1,091 ! Aay30337 Protein encoded by the human DLC-1  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(F)XG  
401: NGSVN WRTGSFHG PGHIS  
AAY31650 ck: 884 len: 530 ! Aay31650 Brevibacterium flavum mutant D-3-P  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
132: LREGE WKRSSFNG VEIFG  
AAY31651 ck: 6831 len: 345 ! Aay31651 Corynebacterium glutamicum D-3-pho  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
132: LREGE WKRSSFNG VEIFG  
AAY31649 ck: 644 len: 530 ! Aay31649 Brevibacterium flavum wild-type D-  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
132: LREGE WKRSSFNG VEIFG

AAY38430 ck: 5842 len: 212 ! Aay38430 Human secreted protein. 9/1999  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
30: TALPQ WRIYSYAG DNIVT  
AAY38421 ck: 4249 len: 71 ! Aay38421 Human secreted protein encoded by  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
30: TALPQ WRIYSYAG DNIVT  
AAY36134 ck: 9084 len: 230 ! Aay36134 Human secreted protein #6. 9/1999  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(Y)XG  
30: MLLPS WKTSSYVG ASIVT  
AAY36181 ck: 8102 len: 230 ! Aay36181 Human secreted protein #53. 9/1999  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(Y)XG  
30: MLLPS WKTSSYVG ASIVT  
AAY06346 ck: 8232 len: 84 ! Aay06346 EGIII-like cellulase (partial sequ  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(Y)XG  
54: STDST WKWKSYSY SNIVA  
AAY22645 ck: 6831 len: 345 ! Aay22645 3-PGDH protein, also known as sera  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
132: LREGE WKRSSFNG VEIFG  
AAY22646 ck: 644 len: 530 ! Aay22646 Wild type 3-PGDH protein, also kno  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
132: LREGE WKRSSFNG VEIFG  
AAY22647 ck: 884 len: 530 ! Aay22647 Mutant 3-PGDH protein, also known  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
132: LREGE WKRSSFNG VEIFG  
AAY34536 ck: 9824 len: 951 ! Aay34536 Porphyromonas gingivalis protein P  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
576: GMFKP WKPPSPGG NLIMI  
AAY34403 ck: 6251 len: 953 ! Aay34403 Porphyromonas gingivalis protein P  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
578: GMFKP WKPPSPGG NLIMI  
AAY13939 ck: 1473 len: 220 ! Aay13939 Human transmembrane protein, HP014:







1	✓	AAB06530	ck: 4356 len: 10	! Aab06530 Claudin-2 cyclic cell adhesion rec	1	2:	C	WRTSSYVG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(S)(Y)XG	C	1	2:	D	WRVSAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06628	ck: 4101 len: 10	! Aab06628 Claudin-3 cyclic cell adhesion rec	
1	✓	AAB06539	ck: 4374 len: 10	! Aab06539 Claudin-2 cyclic cell adhesion rec	1	2:	K	WRTSSYVG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(S)(Y)XG	D	1	2:	E	WRVSAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06636	ck: 2665 len: 8	! Aab06636 Claudin-3 cyclic cell adhesion rec	
1	✓	AAB06548	ck: 4384 len: 10	! Aab06548 Claudin-2 cyclic cell adhesion rec	1	2:	K	WRTSSYVG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(S)(Y)XG	E	1	1:			WRVSAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG		✓	AAB06645	ck: 2669 len: 8	! Aab06645 Claudin-4 cell adhesion recognition
1	✓	AAB06557	ck: 4437 len: 10	! Aab06557 Claudin-2 cyclic cell adhesion rec	1	2:	D	WRTSSYVG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(S)(Y)XG	K	1	2:	C	WRVTAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	C	✓	AAB06654	ck: 4024 len: 10	! Aab06654 Claudin-4 cyclic cell adhesion rec	
1	✓	AAB06566	ck: 4438 len: 10	! Aab06566 Claudin-2 cyclic cell adhesion rec	1	2:	E	WRTSSYVG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(S)(Y)XG	K	1	2:	K	WRVTAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	D	✓	AAB06663	ck: 4042 len: 10	! Aab06663 Claudin-4 cyclic cell adhesion rec	
1	✓	AAB06574	ck: 2954 len: 8	! Aab06574 Claudin-2 cyclic cell adhesion rec	1	1:			W(K,R)XX(S,A)(Y,P)XG W(R)xx(S)(Y)XG		1	2:	K	WRVTAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	✓	AAB06672	ck: 4052 len: 10	! Aab06672 Claudin-4 cyclic cell adhesion rec	
1	✓	AAB06583	ck: 2665 len: 8	! Aab06583 Claudin-3 cell adhesion recognition	1	1:			W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG		1	2:	K	WRVTAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	✓	AAB06681	ck: 4105 len: 10	! Aab06681 Claudin-4 cyclic cell adhesion rec	
1	✓	AAB06592	ck: 4019 len: 10	! Aab06592 Claudin-3 cyclic cell adhesion rec	1	2:	C	WRVSAFIG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(A)(F)XG	C	1	2:	D	WRVTAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06690	ck: 4106 len: 10	! Aab06690 Claudin-4 cyclic cell adhesion rec	
1	✓	AAB06601	ck: 4037 len: 10	! Aab06601 Claudin-3 cyclic cell adhesion rec	1	2:	K	WRVSAFIG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(A)(F)XG	D	1	2:	E	WRVTAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06698	ck: 2669 len: 8	! Aab06698 Claudin-4 cyclic cell adhesion rec	
1	✓	AAB06610	ck: 4047 len: 10	! Aab06610 Claudin-3 cyclic cell adhesion rec	1	2:	K	WRVSAFIG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(A)(F)XG	E	1	1:			WRVTAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG		✓	AAB06764	ck: 2655 len: 8	! Aab06764 Claudin-6/9 cell adhesion recognition
1	✓	AAB06619	ck: 4100 len: 10	! Aab06619 Claudin-3 cyclic cell adhesion rec	1	2:	K	WRVSAFIG	W(K,R)XX(S,A)(Y,P)XG W(R)xx(A)(F)XG	E	1	2:	K	WRVSAFIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	✓	AAB06764	ck: 2655 len: 8	! Aab06764 Claudin-6/9 cell adhesion recognition	

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1: WKVTAFIG
) AAB06772 ck: 4003 len: 10 ! Aab06772 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: C WKVTAFIG C
) AAB06781 ck: 4021 len: 10 ! Aab06781 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: K WKVTAFIG D
) AAB06789 ck: 4031 len: 10 ! Aab06789 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: K WKVTAFIG E
) AAB06798 ck: 4084 len: 10 ! Aab06798 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: D WKVTAFIG K
) AAB06806 ck: 4085 len: 10 ! Aab06806 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: E WKVTAFIG K
) AAB06814 ck: 2655 len: 8 ! Aab06814 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
1: WKVTAFIG
) AAB06911 ck: 4176 len: 10 ! Aab06911 Claudin cell adhesion recognition
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(Y)XG
1: WKIYSYAG DN
) AAB06916 ck: 2655 len: 8 ! Aab06916 Claudin cell adhesion recognition
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
1: WKVTAFIG
) AAY99378 ck: 8102 len: 230 ! Aay99378 Human PRO1356 (UNQ705) amino acid
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(Y)XG
30: MLLPS WKTSSYVG ASIVT
) AAY99420 ck: 828 len: 205 ! Aay99420 Human PRO1486 (UNQ755) amino acid
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(F)XG
192: NLLGG WKISFPG FLIPP
) AAY99434 ck: 4773 len: 220 ! Aay99434 Human PRO1488 (UNQ757) amino acid
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
30: CALPM WKVTAFIG NSIVV
) AAY84609 ck: 8102 len: 230 ! Aay84609 A human membrane associated organi
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(Y)XG
30: MLLPS WKTSSYVG ASIVT
) AAY51675 ck: 2898 len: 211 ! Aay51675 Murine clodin 1 protein. 6/2000
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(Y)XG
30: TALPQ WKIYSYAG DNIVT
) AAY51676 ck: 6271 len: 230 ! Aay51676 Murine clodin 2 protein. 6/2000
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
30: MLLPN WRTSSYVG ASIVT
) AAY51679 ck: 7312 len: 219 ! Aay51679 Murine clodin 3 protein. 6/2000
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
29: CALPM WRVSAFIG SSIT
) AAY51681 ck: 3382 len: 219 ! Aay51681 Murine clodin 6 protein. 6/2000
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
30: CALPM WKVTAFIG NSIVV
) AAY44794 ck: 5085 len: 379 ! Aay44794 P. pastoris Formaldehyde Dehydroge
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
318: VTGRV WRGCAFGG IKGRT
) AAY44795 ck: 7004 len: 392 ! Aay44795 P. pastoris Formaldehyde Dehydroge
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
318: VTGRV WRGCAFGG IKGRT
) AAY68679 ck: 2066 len: 211 ! Aay68679 A human molecule associated with
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
30: TALPQ WKIYSYAG DNIVT
) AAY76130 ck: 5842 len: 212 ! Aay76130 Human secreted protein encoded by
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
30: TALPQ WKIYSYAG DNIVT
) AAY53588 ck: 8341 len: 381 ! Aay53588 Hepatitis B virus surface antigen
W(K,R)XX(S,A)(Y,F)XG

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320: VTGRT	W(K,R)XX(A)(F)XG WKGAAFGG	VKGRS	1	ABP41791	ck: 8440	len: 268	! Abp41791 Human ovarian antigen HSYBI49, SEQ
✓	ABP53938	ck: 3468	len: 9	! Abp53938 VEGFR-3 binding peptide SEQ ID NO: 1	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	WRIYSYAG	DNIVT
2: R	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG WRGNAYPG			ABP41820	ck: 8565	len: 210	! Abp41820 Human ovarian antigen HOGCS42, SEQ
ABG5890	ck: 8102	len: 230	! Abg5890 Human secreted/transmembrane protein	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	WRVTAFIG	SNIVT	
30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT		AAE22226	ck: 7634	len: 230	! Aae22226 Human claudin-D2 protein. 7/2002
ABG96301	ck: 6154	len: 209	! Abg96301 Human ovarian cancer marker M360.	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	WKTSSYVG	ASIVT	
30: CALPM	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG WRVTAFIG	SNIVT		AAE22228	ck: 63	len: 224	! Aae22228 Human claudin-D17 protein. 7/2002
ABP67991	ck: 8102	len: 230	! Abp67991 Human colon cancer related polypeptide	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	WRVSAFVG	SNIVV	
30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT		ABB95518	ck: 8102	len: 230	! Abb95518 Human angiogenesis related protein
ABP65274	ck: 595	len: 569	! Abp65274 Bifidobacterium longum NCC2705 ORF	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	WKTSSYVG	ASIVT	
334: LMIFP	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG WRVPAPAG	LPSPS		ABB95541	ck: 4773	len: 220	! Abb95541 Human angiogenesis related protein
ABB81045	ck: 2784	len: 8	! Abb81045 Pab fragment directed against claudin-1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKIYSYAG	WKVTAFIG	NSIVV	
1:	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKIYSYAG			AAO20543	ck: 3152	len: 211	! Aao20543 Human Claudin-1 protein. 6/2002
AAO15425	ck: 1066	len: 205	! Aao15425 Human genset metabolic gene (GMG-1)	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	WKYSSFSG	FLIFP	
192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG			ABG64505	ck: 9468	len: 140	! Abg64505 Human albumin fusion protein #1180
ABG64505	ck: 9468	len: 140	! Abg64505 Human albumin fusion protein #1180	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	WKTSSYVG	ASIVT	
30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT		ABG64507	ck: 8102	len: 230	! Abg64507 Human albumin fusion protein #1182
ABG64507	ck: 8102	len: 230	! Abg64507 Human albumin fusion protein #1182	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	WKTSSYVG	ASIVT	
30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT		ABP41557	ck: 5827	len: 401	! Abp41557 Human ovarian antigen HVCAC71, SEQ
ABP41557	ck: 5827	len: 401	! Abp41557 Human ovarian antigen HVCAC71, SEQ	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGTAFFG	WKTSSYVG	WKSVE	
341: VTGRT	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGTAFFG			AAU76534	ck: 8102	len: 230	! Aau76534 Tumour-associated antigenic target



1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	AAU10875	ck: 9502	len: 1,173	! Aaul0875	Penicillium citrinum HMG-CoA reduc
1	ABB90240	ck: 9468	len: 140	! Abb90240	Human polypeptide	SEQ ID NO 2616.		
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	97: GPONG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKQSFPG	DADVL		
1	ABB91999	ck: 1756	len: 303	! Abb91999	Herbicidally active polypeptide	SEQ ID NO 301		
1	15: IPGPK	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRKVAYGG	MQIGY	3,952: NVTLK	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG WKPEYDG	GSKIT		
1	ABB93775	ck: 275	len: 895	! Abb93775	Herbicidally active polypeptide	SEQ ID NO 301		
1	621: RSQSQ	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKVVSFAG	LPHFT	6: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTSSYVG	A		
1	ABB84912	ck: 8102	len: 230	! Abb84912	Human PRO1356 protein	sequence		
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	5,614: SCMLN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRPPSYDG	GLKVS		
1	ABB84935	ck: 4773	len: 220	! Abb84935	Human PRO1488 protein	sequence		
1	30: CALPM	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKVTAFIG	NSIVV	ABB62511	ck: 1032	len: 379	! Abb62511	Drosophila melanogaster polypeptid
1	AAU76231	ck: 2066	len: 211	! Aau76231	Human senescence associated	epitope		
1	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRIYSYAG	DNIVT	319: VVGRV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKGSAFAG	WRSVS		
1	AAU83691	ck: 4773	len: 220	! Aau83691	Human PRO protein,	Seq ID No 200.		
1	30: CALPM	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKVTAFIG	NSIVV	8: PGSSP	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRPWAFRG	SSTTR		
1	ABB04707	ck: 8102	len: 230	! Abb04707	Human SP82 protein	SEQ ID NO:2. 3/		
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	ABG00160	ck: 8660	len: 60	! Abg00160	Novel human diagnostic protein #15
1	AAU10521	ck: 8182	len: 230	! Aau10521	Human CAS981 polypeptide.	2/2002		
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	275: ARNTS	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRPNAPFG	YDLS		
1	AAU10522	ck: 6271	len: 230	! Aau10522	Murine CAS81 polypeptide.	2/2002		
1	30: MLLPN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTSSYVG	ASIVT	ABG04118	ck: 4411	len: 437	! Abg04118	Novel human diagnostic protein #41
1	30: MLLPN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTSSYVG	ASIVT	225: SOKPC	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG WKAXAYPG	SGTOR		
1	30: MLLPN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTSSYVG	ASIVT	ABG07792	ck: 7746	len: 731	! Abg07792	Novel human diagnostic protein #77



1	AAU27640	ck: 1615	len: 237	! Aau27640 Human protein APF674834. 12/2001	W(K,R)XX(S,A) (Y,F)XG W(R)xx(A) (Y)XG	4: MAL WRGSAYAG	FLALA	30: CALPM W(K,R)XX(S,A) (F)XG WKVTAFIG	NSIVV	30: CALPM W(K,R)XX(S,A) (F)XG WKVTAFIG	NSIVV	
1	AAU29074	ck: 2066	len: 211	! Aau29074 Human PRO polypeptide sequence #51	W(K,R)XX(S,A) (Y,F)XG W(R)xx(S) (Y)XG	30: TALPQ WRIYSYAG	DNIVT	30: TALPQ W(K,R)XX(S,A) (Y,F)XG WKQSSYAG	DASIQ	30: TALPQ W(K,R)XX(S,A) (Y,F)XG WKQSSYAG	DASIQ	
1	AAU29190	ck: 828	len: 205	! Aau29190 Human PRO polypeptide sequence #16	W(K,R)XX(S,A) (Y,F)XG W(K)xx(S) (F)XG	192: NLLGG WKYSSPSG	FLIPP	60: MLLPS W(K,R)XX(S,A) (Y,F)XG WKTSSYVG	ASIVT	60: MLLPS W(K,R)XX(S,A) (Y,F)XG WKTSSYVG	ASIVT	
1	AAU30271	ck: 5790	len: 219	! Aau30271 Novel human secreted protein #762	W(K,R)XX(S,A) (Y,F)XG W(R)xx(A) (F)XG	140: SEFNP WRLHAFPG	TKPPG	379: EMGLC W(K,R)XX(S,A) (Y,F)XG WKEVAYLG	NEVSD	379: EMGLC W(K,R)XX(S,A) (Y,F)XG WKEVAYLG	NEVSD	
1	AAM57448	ck: 709	len: 5,701	! Aam57448 Human brain expressed single exon	W(K,R)XX(S,A) (Y,F)XG W(K)xx(A) (Y)XG	3,952: NVTLK WKKPAYDG	GSKIT	45: CALPM W(K,R)XX(S,A) (Y,F)XG WKVTAFIG	NSIVV	45: CALPM W(K,R)XX(S,A) (Y,F)XG WKVTAFIG	NSIVV	
1	AAM69843	ck: 709	len: 5,701	! Aam69843 Human bone marrow expressed probe	W(K,R)XX(S,A) (Y,F)XG W(K)xx(A) (Y)XG	3,952: NVTLK WKKPAYDG	GSKIT	AAU42193 ck: 7435	len: 126	! Aam42193 Human polypeptide SEQ ID NO 7124	W(K,R)XX(S,A) (Y,F)XG W(K)xx(S) (Y)XG WKQSSYAG	DASIQ
1	AAM79149	ck: 6092	len: 643	! Aam79149 Human protein SEQ ID NO 1811. 11/2	W(K,R)XX(S,A) (Y,F)XG W(K)xx(A) (F)XG	632: TLEKR WKLCAPEG	IKTT	AAU12417 ck: 8102	len: 230	! Aau12417 Human PRO1356 polypeptide sequence	W(K,R)XX(S,A) (Y,F)XG W(K)xx(A) (Y)XG WKTSSYVG	ASIVT
1	AAM25829	ck: 7435	len: 126	! Aam25829 Human protein sequence SEQ ID NO:1	W(K,R)XX(S,A) (Y,F)XG W(K)xx(S) (Y)XG	73: TALPQ WKQSSYAG	DASIQ	AAU05328 ck: 709	len: 5,701	! Aam05328 Peptide #4010 encoded by probe for	W(K,R)XX(S,A) (Y,F)XG W(K)xx(A) (Y)XG WKKPAYDG	GSKIT
1	AAM38857	ck: 7846	len: 230	! Aam38857 Human polypeptide SEQ ID NO 2002	W(K,R)XX(S,A) (Y,F)XG W(K)xx(S) (Y)XG	30: MLLPS WKTSSYVG	ASIVT	AAB84682 ck: 3601	len: 434	! Aab84682 Nucleotide sequence of a cytidine	W(K,R)XX(S,A) (Y,F)XG W(K)xx(A) (Y)XG WKEVAYLG	NEVSD
1	AAM39319	ck: 2647	len: 434	! Aam39319 Human polypeptide SEQ ID NO 2464	W(K,R)XX(S,A) (Y,F)XG W(K)xx(A) (Y)XG	365: EMGLC WKEVAYLG	NEVSD	AAG90433 ck: 387	len: 275	! Aag90433 C glutamicum protein fragment SEQ	W(K,R)XX(S,A) (Y,F)XG W(K)xx(A) (Y)XG WKDLAYAG	VIDSG
1	AAM39937	ck: 5150	len: 220	! Aam39937 Human polypeptide SEQ ID NO 3082	W(K,R)XX(S,A) (Y,F)XG			130: AAVIG				

1	AAG90500	ck: 6981	len: 301	! Aag90500 C glutamicum protein fragment SEQ	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	365: EMGLC WKEVAYLG	NEVSD	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	! Aab71661 Human colon associated protein #9.
1	254: AGRNW	WKLISFTG	IGSVV		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG	! Aab71661 Human colon associated protein #9.
1	AAG91161	ck: 9818	len: 530	! Aag91161 C glutamicum protein fragment SEQ	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	13: RDSGR WREVSFFG	ETERA	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG	! Aab87565 Human PRO1356. 5/2001
1	132: LREGE	WKGSSPFG	VEIFG		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	! Aab87565 Human PRO1356. 5/2001
1	AAB82494	ck: 2905	len: 376	! Aab82494 Rhodobacter sphaeroides formaldehy	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	! Aab88319 Human membrane or secretory protei
1	316: VTGRV	WKGSAFPG	ARGRT		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	30: MLLPS WKTSSYVG	ASIVT	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab88319 Human membrane or secretory protei
1	AAG75467	ck: 8565	len: 210	! Aag75467 Human colon cancer antigen protein	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	30: CALPM WKVTAFIG	NSIVV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab88319 Human membrane or secretory protei
1	31: CALPM	WRVTAFIG	SNIVT		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab88342 Human membrane or secretory protei
1	AAG81335	ck: 587	len: 496	! Aag81335 Human APP protein sequence SEQ ID	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	30: MLLPS WKTSSYVG	ASIVT	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	! Aab88466 Human membrane or secretory protei
1	4: MAL	WRGSAYAG	FLALA		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	4: MAL WRGSAYAG	FLALA	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	! Aab88466 Human membrane or secretory protei
1	AAE04207	ck: 8102	len: 230	! Aae04207 Human gene 10 encoded secreted pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	30: MLLPS	WKTSSYVG	ASIVT		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	30: MLLPS WKTSSYVG	ASIVT	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	AAE04228	ck: 9468	len: 140	! Aae04228 Human gene 10 encoded secreted pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	! Aab66169 Protein of the invention #81. 4/20
1	30: MLLPS	WKTSSYVG	ASIVT		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	192: NLLGG WKYSSPFG	FLIFP	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	! Aab66183 Protein of the invention #95. 4/20
1	AAE04281	ck: 5423	len: 113	! Aae04281 Human gene 10 encoded secreted pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab50968 Human PRO1488 protein. 3/2001
1	3: PS	WKTSSYVG	ASIVT		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	30: CALPM WKVTAFIG	NSIVV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab50968 Human PRO1488 protein. 3/2001
1	AAE04286	ck: 432	len: 56	! Aae04286 Human gene 10 encoded secreted pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab64401 Amino acid sequence of human intra
1	6: MLLPS	WKTSSYVG	ASIVT		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	30: CALPM WKVTAFIG	NSIVV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab64401 Amino acid sequence of human intra
1	AAB92516	ck: 6755	len: 643	! Aab92516 Human protein sequence SEQ ID NO:1	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab95213 Human protein sequence SEQ ID NO:1
1	632: TLEKR	WKLCAPEG	IKTT		1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab95213 Human protein sequence SEQ ID NO:1
1	AAB95213	ck: 2647	len: 434	! Aab95213 Human protein sequence SEQ ID NO:1	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	30: CALPL WKVTAFIG	NSIVV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	! Aab95213 Human protein sequence SEQ ID NO:1

1	ABR47946	ck: 8102	len: 230	! ABR47946 Human secreted protein, SEQ ID 837	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKTSSYVG	ASIVT	192: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKYSSFSG	FLIPP	1
1	30: MLLPS									
1	ABR48131	ck: 9468	len: 140	! ABR48131 Human secreted protein, SEQ ID 102	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRIYSYAG	DNIVT	1
1	30: MLLPS									
1	ABG74786	ck: 2447	len: 31,267	! ABG74786 Human RGS11 protéin. 6/2003	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT	192: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKYSSFSG	FLIPP	1
1	22,972: NVTLK									
1	ABU71162	ck: 2066	len: 211	! ABU71162 Human PRO944 protein. 6/2003	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WKKPAYDG	GSKIT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT	1
1	30: TALPQ									
1	ABU71278	ck: 828	len: 205	! ABU71278 Human PRO1486 protein. 6/2003	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKYSSFSG	FLIPP	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRIYSYAG	DNIVT	1
1	30: CALPM									
1	ABU71434	ck: 4773	len: 220	! ABU71434 Human neoplasia inhibiting PRO pol	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKVTAFIG	NSIVV	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRIYSYAG	DNIVT	1
1	30: MLLPS									
1	ABU71545	ck: 8102	len: 230	! ABU71545 Human secreted polypeptide PRO1356	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKYSSFSG	FLIPP	1
1	30: MLLPS									
1	ABU71991	ck: 8102	len: 230	! ABU71991 Novel human secreted and transmembr	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT	1
1	30: MLLPS									
1	ABU72148	ck: 8102	len: 230	! ABU72148 Human PRO polypeptide #40. 6/2003	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSYVG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRIYSYAG	DNIVT	1
1	30: MLLPS									
1	ABU65619	ck: 2066	len: 211	! ABU65619 Human secreted/transmembrane prote	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WKTSSYVG	ASIVT	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRIYSYAG	DNIVT	1
1	30: TALPQ									
1	ABU65735	ck: 828	len: 205	! ABU65735 Human secreted/transmembrane prote	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG					1



107: HLFY W(R)xx(A) (Y) xG YEEAI  
WRMLAYKG

Databases searched:  
Geneseq-AA, Release 13.0, Released on 19Jun2003, Formatted on 15Jul2003

Total finds: 271  
Total length: 158,726,570  
Total sequences: 1,107,863  
CPU time: 05:28.43

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2004, 08:21:38 ; Search time 27 Seconds  
(without alignments)  
12.537 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 61971

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	56.5	8	US-09-324-541-11	Sequence 11, Appl
2	12	52.2	8	US-08-469-260A-564	Sequence 564, App
3	12	52.2	8	US-08-488-446-564	Sequence 564, App
4	12	52.2	8	US-08-467-344A-564	Sequence 564, App
5	11	47.8	2	US-08-415-099A-1	Sequence 1, Appl
6	11	47.8	2	US-08-451-822A-19	Sequence 19, Appl
7	11	47.8	3	US-07-858-842-5	Sequence 5, Appl
8	11	47.8	3	US-07-960-636B-4	Sequence 4, Appl
9	11	47.8	3	US-08-165-545-4	Sequence 4, Appl
10	11	47.8	3	US-08-165-545-8	Sequence 8, Appl
11	11	47.8	3	US-08-165-545-12	Sequence 12, Appl
12	11	47.8	3	US-08-305-768-27	Sequence 27, Appl
13	11	47.8	3	US-08-256-771-13	Sequence 13, Appl
14	11	47.8	3	US-08-256-771-17	Sequence 17, Appl
15	11	47.8	3	US-08-256-771-21	Sequence 21, Appl
16	11	47.8	3	US-08-433-037-14	Sequence 14, Appl
17	11	47.8	3	US-08-440-504A-1	Sequence 1, Appl
18	11	47.8	3	US-08-381-984-13	Sequence 13, Appl
19	11	47.8	3	US-08-381-984-17	Sequence 17, Appl
20	11	47.8	3	US-08-381-984-21	Sequence 21, Appl
21	11	47.8	3	US-08-871-163-27	Sequence 27, Appl
22	11	47.8	3	US-08-685-589A-89	Sequence 89, Appl
23	11	47.8	3	US-08-685-589A-90	Sequence 90, Appl
24	11	47.8	3	US-08-685-589A-92	Sequence 92, Appl
25	11	47.8	3	US-08-685-589A-93	Sequence 93, Appl
26	11	47.8	3	US-08-685-589A-94	Sequence 94, Appl
27	11	47.8	3	US-08-767-903-27	Sequence 27, Appl

28	11	47.8	3	US-08-590-897A-25	Sequence 25, Appl
29	11	47.8	3	US-08-433-613-1	Sequence 1, Appl
30	11	47.8	3	US-09-461-697-291	Sequence 291, App
31	11	47.8	3	US-09-461-697-405	Sequence 405, App
32	11	47.8	3	US-08-871-561-44	Sequence 44, Appl
33	11	47.8	3	US-09-167-513-6	Sequence 6, Appl
34	11	47.8	3	US-09-149-476-525	Sequence 525, App
35	11	47.8	3	PCT-US95-11724-27	Sequence 27, Appl
36	11	47.8	4	US-07-801-388-6	Sequence 6, Appl
37	11	47.8	4	US-08-061-065-6	Sequence 6, Appl
38	11	47.8	4	US-07-938-436-1	Sequence 1, Appl
39	11	47.8	4	US-07-932-200-1	Sequence 1, Appl
40	11	47.8	4	US-08-159-617-7	Sequence 7, Appl
41	11	47.8	4	US-07-841-997A-32	Sequence 32, Appl
42	11	47.8	4	US-08-165-545-3	Sequence 3, Appl
43	11	47.8	4	US-08-165-545-6	Sequence 6, Appl
44	11	47.8	4	US-08-165-545-7	Sequence 7, Appl
45	11	47.8	4		

ALIGNMENTS

RESULT 1  
US-09-324-541-11  
; Sequence 11, Application US/09324541  
; Patent No. 6391855  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: JUNCTIONAL ADHESION MOLECULE-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.412  
; CURRENT APPLICATION NUMBER: US/09/324,541  
; CURRENT FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fab fragment directed against claudin cell  
; OTHER INFORMATION: adhesion recognition sequence  
US-09-324-541-11

Query Match 56.5%; Score 13; DB 4; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.5e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 1 WKIYSYAG 8

RESULT 2  
US-08-469-260A-564  
; Sequence 564, Application US/08469260A  
; Patent No. 6451578  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATTIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHROFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A. NON-B. NON-C. NON-D. NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716



CORRESPONDENCE ADDRESS:  
ADDRESSES: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,260A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-260A-564

Query Match 52.2%; Score 12; DB 4; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.5e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 1 WWSGLGG 8

RESULT 3  
US-08-488-446-564  
Sequence 564, Application US/08488446  
Patent No. 6558898  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATTIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUERHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESS: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 564:  
US-08-467-344A-564

Query Match 52.2%; Score 12; DB 4; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.5e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXX 8  
Db 1 WHSGLGG 8

RESULT 5  
US-08-415-099A-1

; Sequence 1, Application US/08415099A  
; Patent No. 5789384

; GENERAL INFORMATION:

; APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.

; TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Thereof"

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cytovent

; STREET: 10230 N.E. Points Drive, Suite 530

; CITY: Kirkland

; STATE: Washington

; COUNTRY: USA

; ZIP: 98033

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette-3.25 inch, 1.44mb storage

; COMPUTER: IBM PC/486 Compatible

; OPERATING SYSTEM: MS-DOS 5.01

; SOFTWARE: Word for Windows 6.0-t

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/415,099A

; FILING DATE: 31-MAR-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,386

; FILING DATE: 06-JUL-1994

; APPLICATION NUMBER: 08/026,341

; FILING DATE: March 4, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Sundemo, John S.

; REGISTRATION NUMBER: 34,446

; REFERENCE/DOCKET NUMBER: 15548-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 1-206-889-5804(direct)

; TELEFAX: 1-206-822-3644

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2 amino acids

; TYPE: AMINO

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

US-08-415-099A-1

Query Match 47.8%; Score 11; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 2 W 2

## RESULT 6

US-08-451-822A-19

; Sequence 19, Application US/08451822A

; Patent No. 5863888

; GENERAL INFORMATION:

; APPLICANT: Dionne, Craig A

; APPLICANT: Crumley, Greg

; APPLICANT: Jaye, Michael C

; APPLICANT: Schlensing, Joseph

; TITLE OF INVENTION: Fibroblast Growth Factor Receptors

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Legal Department

; STREET: 500 Arcola Road

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/451,822A

; FILING DATE: 26-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/323,430

; FILING DATE: 14-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/934,372

; FILING DATE: 21-AUG-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/549,587

; FILING DATE: 06-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A0496E

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-3816

; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-451-822A-19

Query Match 47.8%; Score 11; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 1 W 1

## RESULT 7

US-07-858-842-5

; Sequence 5, Application US/07858842

; Patent No. 5314807

; GENERAL INFORMATION:

; APPLICANT: Yoshikawa, Masaaki

; APPLICANT: Yokoyama, Keiichi

; APPLICANT: Hasegawa, Masayasu

; APPLICANT: Yasumoto, Ryouchi

; APPLICANT: Fujita, Hiroyuki

us-09-185-908-1.slim8.ra1

Mon Jan 12 08:42:32 2004

TITLE OF INVENTION: METHOD FOR PRODUCING AN ANGIOTENSIN  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ARMSTRONG & KUBOVCIK  
 STREET: 1725 K Street N.W. Suite 1000  
 CITY: Washington  
 STATE: District of Columbia  
 COUNTRY: United States of America  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/858,842  
 FILING DATE: 19920327  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 142283  
 FILING DATE: 29-MAR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 298060  
 FILING DATE: 17-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gormley, Mary E.  
 REGISTRATION NUMBER: 34, 409  
 REFERENCE/DOCKET NUMBER: 920247  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 659-2930  
 TELEFAX: (202) 887-0357  
 TELEX: 440142  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 US-07-858-842-5

Query Match 47.8%; Score 11; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 1 W 1  
 DB 3 W 3

RESULT 8  
 US-07-960-636B-4  
 ; Sequence 4, Application US/07960636B  
 ; Patent No. 5369015  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yoshikawa, Masaaki  
 ; APPLICANT: Yokoyama, Keiichi  
 ; APPLICANT: Hasegawa, Masayasu  
 ; APPLICANT: Yasumoto, Ryouichi  
 ; APPLICANT: Fujita, Hiroyuki  
 ; TITLE OF INVENTION: Method for Producing an Angiotensin  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Armstrong, Westernman, Hattori, McLeland &  
 ; ADDRESSEE: Naughton  
 ; STREET: 1725 K Street, N.W., Suite 1000  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20006  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/960,636B  
 FILING DATE: 14-OCT-1992  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 298061/1991  
 FILING DATE: 17-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Tockman, Albert  
 REGISTRATION NUMBER: 19722  
 REFERENCE/DOCKET NUMBER: F1161-2679-A920798  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 659-2930  
 TELEFAX: (202) 887-0357  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Mammalian meat, fish, crustaceans  
 US-07-960-636B-4

Query Match 47.8%; Score 11; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 1 W 1  
 DB 3 W 3

RESULT 9  
 US-08-165-545-4  
 ; Sequence 4, Application US/08165545  
 ; Patent No. 5424396  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mamoru TOMITA et al.  
 ; TITLE OF INVENTION: Antimicrobial Peptide and  
 ; TITLE OF INVENTION: Antimicrobial Agent  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Wenderoth, Lind & Ponack  
 ; STREET: 805 Fifteenth Street, N.W., #700  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: DisplayWrite  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/165,545  
 ; FILING DATE:  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/871,981  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warren M. Cheek, Jr.  
 ; REGISTRATION NUMBER: 33,367  
 ; REFERENCE/DOCKET NUMBER:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-8850  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-165-545-4

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
DB 1 W 1

RESULT 10  
US-08-165-545-8  
Sequence 8, Application US/08165545  
Patent No. 5424396  
GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptide and  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/165,545  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/871,981  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-165-545-8

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
DB 2 W 2

RESULT 11

us-09-185-908-1.slim8.ra1

Mon Jan 12 08:42:32 2004

US-08-165-545-12  
; Sequence 12, Application US/08165545  
; Patent No. 5424396  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial peptide and  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/165,545  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/871,981  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:

US-08-165-545-12  
; Query Match 47.8%; Score 11; DB 1; Length 3;  
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 2 W 2

RESULT 12  
US-08-305-768-27  
; Sequence 27, Application US/08305768  
; Patent No. 5602097  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Antifungal Peptides  
; NUMBER OF SEQUENCES: 31  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/305,768  
; FILING DATE: 12-SEPT-1994  
; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-305-768-27

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 1 W 1

RESULT 13  
US-08-256-771-13  
; Sequence 13, Application US/08256771  
; Patent No. 5656591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1

US-08-165-545-12  
; Sequence 12, Application US/08165545  
; Patent No. 5424396  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial peptide and  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/165,545  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/871,981  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:

TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid

cy	1	w	1
qb	2	w	2

Search completed: January 12, 2004, 08:26:47  
Job time : 29 secs

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OM protein - protein search, using sw model

Run on: January 12, 2004, 08:25:23 ; Search time 68 Seconds  
(without alignments)  
23.707 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 49186

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pdp:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pdp:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pdp:\*
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- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pdp:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pdp:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pdp:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pdp:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pdp:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pdp:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pdp:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pdp:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pdp:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pdp:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pdp:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pdp:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pdp:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	60.9	8	10	US-09-185-908-42
2	14	60.9	8	10	US-09-185-908-163
3	13	56.5	8	10	US-09-185-908-34
4	13	56.5	8	10	US-09-185-908-50
5	13	56.5	8	10	US-09-185-908-58
6	13	56.5	8	10	US-09-185-908-110
7	13	56.5	8	10	US-09-185-908-216
8	13	56.5	8	10	US-09-185-908-269
9	13	56.5	8	11	US-09-986-480-361
10	13	56.5	8	15	US-10-419-537-11
11	12	52.2	8	8	US-08-424-550B-564
12	12	52.2	8	12	US-10-231-417-485
13	11	47.8	2	15	US-10-197-954-42
14	11	47.8	3	10	US-09-922-261-291
15	11	47.8	3	10	US-09-922-261-405

16	11	47.8	3	10	US-09-982-172-25	Sequence 25, Appl
17	11	47.8	3	11	US-09-809-391-525	Sequence 525, App
18	11	47.8	3	11	US-09-852-910-151	Sequence 151, App
19	11	47.8	3	12	US-10-190-082-239	Sequence 239, App
20	11	47.8	3	12	US-09-882-171-525	Sequence 525, App
21	11	47.8	3	15	US-10-039-876A-6	Sequence 6, Appli
22	11	47.8	4	7	US-08-996-140-6	Sequence 5, Appli
23	11	47.8	4	8	US-08-484-409-5	Sequence 29, Appli
24	11	47.8	4	8	US-08-484-409-29	Sequence 34, Appli
25	11	47.8	4	8	US-08-981-824-43	Sequence 43, Appli
26	11	47.8	4	8	US-08-424-550B-216	Sequence 216, App
27	11	47.8	4	8	US-08-424-550B-314	Sequence 314, App
28	11	47.8	4	8	US-08-424-550B-346	Sequence 346, App
29	11	47.8	4	8	US-08-841-636A-3	Sequence 3, Appli
30	11	47.8	4	9	US-09-736-611-1	Sequence 1, Appli
31	11	47.8	4	9	US-09-736-611-2	Sequence 2, Appli
32	11	47.8	4	9	US-09-765-527-156	Sequence 196, App
33	11	47.8	4	9	US-09-780-070-1	Sequence 1, Appli
34	11	47.8	4	9	US-09-780-070-2	Sequence 2, Appli
35	11	47.8	4	9	US-09-871-212-2	Sequence 2, Appli
36	11	47.8	4	9	US-09-808-037-4	Sequence 4, Appli
37	11	47.8	4	9	US-09-155-076-4	Sequence 4, Appli
38	11	47.8	4	9	US-09-155-076-5	Sequence 5, Appli
39	11	47.8	4	9	US-09-853-918-11	Sequence 11, Appli
40	11	47.8	4	9	US-09-853-918-19	Sequence 19, Appli
41	11	47.8	4	9	US-09-782-980-112	Sequence 112, App
42	11	47.8	4	9	US-09-741-148A-13	Sequence 13, Appl
43	11	47.8	4	9	US-09-682-667-12	Sequence 12, Appl
44	11	47.8	4	9	US-09-682-667-13	Sequence 13, Appl
45	11	47.8	4	9		

## ALIGNMENTS

RESULT 1  
US-09-185-908-42  
; Sequence 42, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; TITLE OF INVENTION: FUNCTIONS  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185.908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence  
US-09-185-908-42

Query Match 60.9%; Score 14; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No; 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 1 WXXXXXXG 8  
|  
Db 1 WRTSSVVG 8

RESULT 2  
US-09-185-908-163  
; Sequence 163, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
FILE REFERENCE: 100086.409  
CURRENT APPLICATION NUMBER: US/09/185,908A  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 269  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 163  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Product of  
OTHER INFORMATION: synthesis based on mouse claudin-2 sequence  
FEATURE:  
OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-163

Query Match 60.9%; Score 14; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 1 WRTSSYVG 8

RESULT 3  
US-09-185-908-34  
Sequence 34, Application US/09185908A  
Publication No. US20020193294A1  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
FILE REFERENCE: 100086.409  
CURRENT APPLICATION NUMBER: US/09/185,908A  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 269  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 34  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Product of  
OTHER INFORMATION: Synthesis based on mouse claudin-1 sequence  
US-09-185-908-34

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 1 WKIYSYAG 8

RESULT 4  
US-09-185-908-50  
Sequence 50, Application US/09185908A  
Publication No. US20020193294A1  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
FILE REFERENCE: 100086.409  
CURRENT APPLICATION NUMBER: US/09/185,908A  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 269

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 50  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Product of  
OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R  
OTHER INFORMATION: sequences  
US-09-185-908-50

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 1 WRVTAPIG 8

RESULT 5  
US-09-185-908-58  
Sequence 58, Application US/09185908A  
Publication No. US20020193294A1  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
FILE REFERENCE: 100086.409  
CURRENT APPLICATION NUMBER: US/09/185,908A  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 269  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 58  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Product of  
OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences  
US-09-185-908-58

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 1 WRVSAFIG 8

RESULT 6  
US-09-185-908-110  
Sequence 110, Application US/09185908A  
Publication No. US20020193294A1  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
FILE REFERENCE: 100086.409  
CURRENT APPLICATION NUMBER: US/09/185,908A  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 269  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 110  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Product of  
OTHER INFORMATION: synthesis based on mouse claudin-1 sequence



FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-110

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
|  
Db 1 WKIYSYAG 8

RESULT 7  
US-09-185-908-216  
; Sequence 216, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; PRIOR FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 216  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-216

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
|  
Db 1 WRVTAPFG 8

RESULT 8  
US-09-185-908-269  
; Sequence 269, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; PRIOR FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 269  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-269

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
|  
Db 1 WRVSAFIG 8

RESULT 9  
US-09-986-480-361  
; Sequence 361, Application US/09986480  
; Publication No. US20030027999A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 143 Human Secreted Proteins  
; FILE REFERENCE: PS500P1  
; CURRENT APPLICATION NUMBER: US/09/986,480  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: PCT/US00/12788  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/134,068  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 456  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 361  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-986-480-361

Query Match 56.5%; Score 13; DB 11; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
|  
Db 1 WGLVTLAG 8

RESULT 10  
US-10-119-537-11  
; Sequence 11, Application US/10119537  
; Publication No. US20030027761A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: 100086.412D1  
; CURRENT APPLICATION NUMBER: US/10/119,537  
; CURRENT FILING DATE: 2002-04-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fab fragment directed against claudin cell  
; OTHER INFORMATION: adhesion recognition sequence  
US-10-119-537-11

Query Match 56.5%; Score 13; DB 15; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
|  
Db 1 WKIYSYAG 8

us-09-185-908-1.slim8.rapb

Mon Jan 12 08:42:33 2004

```

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-417-485

Query Match      52.2%; Score 12; DB 12; Length 8;
Best Local Similarity 25.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 6;

QY      1 WXXXXXXG 8
Db      1 WLLSEKKG 8

RESULT 13
US-10-197-954-42
; Sequence 42, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-42

Query Match      47.8%; Score 11; DB 15; Length 2;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0;

QY      1 W 1
Db      1 W 1

RESULT 14
US-09-922-261-291
; Sequence 291, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 485

US-08-424-550B-564
; Sequence 564, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-NATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 564:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-564

Query Match      52.2%; Score 12; DB 8; Length 8;
Best Local Similarity 25.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 6;

QY      1 WXXXXXXG 8
Db      1 WHSGLLGG 8

RESULT 12
US-10-231-417-485
; Sequence 485, Application US/10231417
; Publication No. US20030176681A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: P20191
; CURRENT APPLICATION NUMBER: US/10/231,417
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/296,622
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 485
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; SEQ ID NO 291  
 ; LENGTH: 3  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-922-261-291

Query Match 47.8%; Score 11; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
 Db 2 W 2

RESULT 15  
 US-09-922-261-405  
 ; Sequence 405, Application US/09922261  
 ; Patent No. US20020111471A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.  
 ; APPLICANT: Lo, Donald C.  
 ; APPLICANT: Barney, Shawn  
 ; APPLICANT: Thomas, Mary Beth  
 ; APPLICANT: Portbury, Stuart D.  
 ; APPLICANT: Puranam, Kasturi  
 ; APPLICANT: Katz, Lawrence C.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
 ; FILE REFERENCE: 10001-005-999  
 ; CURRENT APPLICATION NUMBER: US/09/922,261  
 ; PRIOR FILING DATE: 2001-08-03  
 ; PRIOR APPLICATION NUMBER: US/09/461,697  
 ; PRIOR FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 466  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 405  
 ; LENGTH: 3  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-922-261-405

Query Match 47.8%; Score 11; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
 Db 2 W 2

Search completed: January 12, 2004, 08:34:47  
 Job time : 71 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2004, 08:19:29 ; Search time 82 Seconds

(without alignments)  
25.176 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 452

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	47.8	7	2	Q8KMS9
2	11	47.8	7	2	Q8GL04
3	11	47.8	7	2	Q8GL00
4	11	47.8	7	8	Q95945
5	11	47.8	7	10	O49223
6	11	47.8	7	15	Q8JEB1
7	11	47.8	8	2	O85406
8	11	47.8	8	2	Q8GL21
9	11	47.8	8	2	Q8G940
10	11	47.8	8	4	Q15890
11	11	47.8	8	4	Q15888
12	11	47.8	8	4	Q8IVK3
13	11	47.8	8	5	P82685
14	11	47.8	8	5	P82686
15	11	47.8	8	5	P82687
16	11	47.8	8	5	P82688

17	11	47.8	8	5	P82689
18	11	47.8	8	6	O02831
19	11	47.8	8	6	Q95M23
20	11	47.8	8	6	Q9TRY3
21	11	47.8	8	8	Q8W8G2
22	11	47.8	8	8	Q8W8G4
23	11	47.8	8	8	Q94VC1
24	11	47.8	8	8	Q94VP6
25	11	47.8	8	8	Q8WGD7
26	11	47.8	8	8	Q94V88
27	11	47.8	8	8	Q94V82
28	11	47.8	8	8	Q9TD02
29	11	47.8	8	8	Q9T4Y2
30	11	47.8	8	8	Q94PX5
31	11	47.8	8	8	Q8W8G6
32	11	47.8	8	8	Q8W8G5
33	11	47.8	8	8	Q94VJ4
34	11	47.8	8	8	Q8W8G3
35	11	47.8	8	8	Q94V91
36	11	47.8	8	8	Q94VE4
37	11	47.8	8	8	Q94VE2
38	11	47.8	8	8	Q94VF9
39	11	47.8	8	8	Q94PX7
40	11	47.8	8	8	Q94PX6
41	11	47.8	8	8	Q94VA7
42	11	47.8	8	8	Q94VB5
43	11	47.8	8	11	Q9ET18
44	11	47.8	8	11	Q99MN0
45	11	47.8	8	11	O35835

P82689 periplaneta  
O02831 oryctolagus  
Q95M23 sus scrofa  
Q9TRY3 sus sp. ins  
Q8W8G2 diadema sav  
Q8W8G4 diadema mex  
Q94VC1 varanus rud  
Q94VF6 varanus job  
Q8WGD7 lomus hirta  
Q94V88 varanus tri  
Q94V82 varanus yuw  
Q9TD02 terranatos  
Q9T4Y2 asterina pe  
Q94PX5 felis silve  
Q8W8G6 diadema mex  
Q8W8G5 diadema ant  
Q94VJ4 varanus ben  
Q8W8G3 diadema pau  
Q94V91 varanus tim  
Q94VE4 varanus mel  
Q94VE2 varanus sal  
Q94VF9 varanus ind  
Q94PX7 felis silve  
Q94PX6 felis libyc  
Q94VA7 varanus sal  
Q94VB5 varanus sal  
Q9ET18 mus spretus  
Q99MN0 mus musculus  
O35835 rattus sp.

#### ALIGNMENTS

RESULT 1  
Q8KMS9  
ID Q8KMS9 PRELIMINARY; PRT; 7 AA.  
AC Q8KMS9;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Putative transposase (Fragment).  
GN TNIA.  
OS Enterobacter sp. CH2-4.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=143777;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CH2-4;  
RX MEDLINE=21604134; PubMed=11763242;  
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,  
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,  
RA Yurieva O.V., Nikiforov V.G.;  
RT "Mercury resistance transposons of Gram-negative environmental  
bacteria and their classification";  
RL Res. Microbiol. 152:811-822(2001).  
DR EMBL; AJ302778; CAC83058.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DAA9A0 CRC64;

Query Match 47.8%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
Db 7 W 7

RESULT 2

Q8GL04

ID Q8GL04 PRELIMINARY; PRT; 7 AA.

OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D273-10B;  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system: Structure and  
RT nucleotide sequence of the gene coding for subunit 1 of yeast  
RT cytochrome oxidase";  
RL J. Biol. Chem. 255:11927-11941(1980).  
RW EMBL; V00694; CAA24066.1; -  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;  
Query Match 47.8%; Score 11; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 4 W 4  
RESULT 5  
ID O49223 PRELIMINARY; PRT; 7 AA.  
AC O49223;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HMG-1-like protein (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RX MEDLINE=91367679; PubMed=1891369;  
RA Laux T., Goldberg R.B.;  
RT "A plant DNA binding protein shares highly conserved sequence motifs  
RT with HMG-box proteins";  
RL Nucleic Acids Res. 19:4769-4769(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RA Mahalingam R., Knap H.T.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF047050; RAC03556.1; -  
FT NON TER 1  
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;  
Query Match 47.8%; Score 11; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 2 W 2  
RESULT 6  
ID Q8JE81 PRELIMINARY; PRT; 7 AA.  
AC Q8JE81;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-5.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=93-0107;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
RT prophages: conservation amidst diversity";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142103; AANI7848.1; -  
KW Plasmid.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 914 MW; 6337244330504310 CRC64;  
Query Match 47.8%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 1 W 1  
RESULT 3  
ID Q8GL00 PRELIMINARY; PRT; 7 AA.  
AC Q8GL00;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE PF-50 protein (Fragment).  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-13.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CA15;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
RT prophages: conservation amidst diversity";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142106; AANI7857.1; -  
FT NON TER 1  
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;  
Query Match 47.8%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 2 W 2  
RESULT 4  
ID Q95945 PRELIMINARY; PRT; 7 AA.  
AC Q95945;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Inside intron 5 (Fragment).

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Truncated pol protein (Fragment).  
GN POL.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=4874;  
RC MEDLINE=22056123; PubMed=12060770;  
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,  
RA Hofmann D., Korn K., Seibig J.;  
RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics  
RT approach to predicting phenotype from genotype.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).  
DR EMBL; AF347267; AAK32344.1; -;  
FT NON TER 1  
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;  
  
Query Match 47.8%; Score 11; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 6 W 6

RESULT 7  
O85406 PRELIMINARY; PRT; 8 AA.  
ID O85406  
AC O85406;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Hypothetical 1.0 kDa protein (Fragment).  
OS Coccidia burnetii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
OC Coxiellaceae; Coxiella.  
OX NCBI\_TaxID=777;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Nine Mile Phase I;  
RX MEDLINE=98348442; PubMed=9683477;  
RA Williams H., Jaeger C., Baljer G.;  
RT "Physical and genetic map of the obligate intracellular bacterium  
RT Coxiella burnetii";  
RL J. Bacteriol. 180:3816-3822(1998).  
DR EMBL; AF064963; AAD09947.1; -;  
FT NON TER 1  
SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match 47.8%; Score 11; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 4 W 4

RESULT 8  
O8GL21 PRELIMINARY; PRT; 8 AA.  
ID O8GL21  
AC O8GL21;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE PP-50 protein (Fragment).  
GN PP-50.  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-8.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sh-2-82;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
RT prophages: conservation amidst diversity.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142094; AAN17903.1; -;  
FT NON TER 1  
SQ SEQUENCE 8 AA; 1042 MW; 1437244337204373 CRC64;  
  
Query Match 47.8%; Score 11; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 2 W 2

RESULT 9  
O8G940 PRELIMINARY; PRT; 8 AA.  
ID O8G940  
AC O8G940;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE PP-50 protein (Fragment).  
GN PP-50.  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-9, and Plasmid group cp32-12.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DNI27c19-2, and Sh-2-82;  
RC PLASMID-group cp32-9, and group cp32-12;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
RT prophages: conservation amidst diversity.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142104; AAN17853.1; -;  
DR EMBL; AY142097; AAN17907.1; -;  
FT NON TER 1  
SQ SEQUENCE 8 AA; 1042 MW; 1437244330504373 CRC64;

Query Match 47.8%; Score 11; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 2 W 2

RESULT 10  
Q15890 PRELIMINARY; PRT; 8 AA.  
ID Q15890  
AC Q15890;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE (Clone XP19C12A) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

TISSUE-Placenta;  
 Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries."  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32083; AAA73880.1; --  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 975 MW; 605EAC65BEA5A2D3 CRC64;  
 Query Match 47.8%; Score 11; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 W 1  
 DB 1 W 1

RESULT 11  
 Q15888 PRELIMINARY; PRT; 8 AA.  
 ID Q15888  
 AC Q15888  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE (Clone XP15H8A) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries."  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32069; AAA73878.1; --  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;  
 Query Match 47.8%; Score 11; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 W 1  
 DB 6 W 6

RESULT 12  
 Q81VK3 PRELIMINARY; PRT; 8 AA.  
 ID Q81VK3  
 AC Q81VK3  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Steerin2 (Fragment).  
 GN STEERIN2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,  
 RA Gysen J.J.G.H.;

RT "Sensorineural defects in mice hypomorphic for a mammalian homolog of  
 RT unc-53";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases..  
 DR EMBL; AJ488208; CAD32561.1; --  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;  
 Query Match 47.8%; Score 11; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 W 1  
 DB 3 W 3

RESULT 13  
 P82685 PRELIMINARY; PRT; 8 AA.  
 ID P82685  
 AC P82685  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE Kinin-1 (PEA-K-1)  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattellidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=CORPORA CARDIACA;  
 RX MEDLINE=98010462; PubMed=9350979;  
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of eight kinins from the  
 RT retrocerebral complex of the American cockroach, Periplaneta  
 RT americana.";  
 RL Regul. Pept. 71:199-205(1997).  
 CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC -|- (MYOTROPIC ACTIVITY).  
 CC -|- SIMILARITY: BELONGS TO THE KININ FAMILY.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 8 8  
 FT MOD RES 8 8  
 FT SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;  
 SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;  
 Query Match 47.8%; Score 11; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 W 1  
 DB 7 W 7

RESULT 14  
 P82686 PRELIMINARY; PRT; 8 AA.  
 ID P82686  
 AC P82686  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE Kinin-2 (PEA-K-2).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattellidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=CORPORA CARDIACA;  
 RX MEDLINE=98010462; PubMed=9350979;  
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of eight kinins from the

RT retrocerebral complex of the American cockroach, Periplaneta  
RT americana";

RL Regul. Pept. 71:199-205(1997).

CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC -|- (MYOTROPIC ACTIVITY).

CC -|- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.

FT MOD RES 8 8

SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;

Query Match

Best Local Similarity 47.8%; Score 11; DB 5; Length 8;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1

Db 7 W 7

# RESULT 15

P82687

ID P82687 PRELIMINARY; PRT; 8 AA.

AC P82687;

DT 01-MAR-2001 (TREMELrel. 16, Created)

DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)

DE Kinin-3 (PEA-K-3).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;

OC Blattellidae; Periplaneta.

OX NCBI TaxID=6978;

RN [1]

RP SEQUENCE AND FUNCTION.

RC TISSUE=CORPORA CARDIACA;

RX MEDLINE=98010462; PubMed=9350979;

RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;

RT "Isolation and structural elucidation of eight kinins from the

RT retrocerebral complex of the American cockroach, Periplaneta

RT americana";

RL Regul. Pept. 71:199-205(1997).

CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC -|- (MYOTROPIC ACTIVITY).

CC -|- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.

FT MOD RES 8 8

SQ SEQUENCE 8 AA; 909 MW; DC6365B49D5A76A CRC64;

Query Match

Best Local Similarity 47.8%; Score 11; DB 5; Length 8;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1

Db 7 W 7

Search completed: January 12, 2004, 08:25:14

Job time : 85 secs



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OM protein - protein search, using sw model

Run on: January 12, 2004, 08:11:53 ; Search time 72 seconds  
(without alignments)  
17.636 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 102276

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :			
A_Geneseq 15Jun03.*			
1:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*		
2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*		
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*		
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6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*		
7:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*		
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22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*		
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*		
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	14	60.9	8	21	AA06521
2	14	60.9	8	21	AA06574
3	14	60.9	8	21	AA06823
4	14	60.9	8	21	AA06876
5	14	60.9	8	21	AA06917
6	13	56.5	8	21	AA06267
7	13	56.5	8	21	AA06419
8	13	56.5	8	21	AA06426
9	13	56.5	8	21	AA06479

10	13	56.5	8	21	AA06512	Claudin-1 cyclic c
11	13	56.5	8	21	AA06583	Claudin-3 cell adh
12	13	56.5	8	21	AA06636	Claudin-3 cyclic c
13	13	56.5	8	21	AA06645	Claudin-4 cell adh
14	13	56.5	8	21	AA06698	Claudin-4 cyclic c
15	13	56.5	8	21	AA06764	Claudin-6/9 cell a
16	13	56.5	8	21	AA06814	Claudin-6/9 cyclic
17	13	56.5	8	21	AA06916	Claudin cell adhes
18	13	56.5	8	21	AA07768	Hyaluronic acid (H
19	13	56.5	8	22	AA05108	Dopamine transport
20	13	56.5	8	23	AB01045	Fab fragment direc
21	12	52.2	8	20	AA19720	SEQ ID NO 438 from
22	12	52.2	8	21	AA09437	Hepatitis GB virus
23	12	52.2	8	23	AB10684	Japanese encephali
24	11	47.8	8	22	AA07814	Human peptide #108
25	11	47.8	2	22	AA09874	Human peptide #202
26	11	47.8	2	22	AA09140	Tachykinins peptid
27	11	47.8	2	22	AA09156	Endothelins and re
28	11	47.8	2	22	AA09173	Opioid peptide SEQ
29	11	47.8	2	23	AB06385	Human albumin fusi
30	11	47.8	2	24	AB04810	Binding receptor w
31	11	47.8	3	10	AA09098	Sequence of fragme
32	11	47.8	3	11	AA09798	Partial sequence o
33	11	47.8	3	11	AA05915	Triptide inhibit
34	11	47.8	3	15	AA05949	ACE-inhibitor SP3.
35	11	47.8	3	15	AA04256	GHRP-6 analog. Sy
36	11	47.8	3	15	AA04753	Lactoferrin derive
37	11	47.8	3	15	AA04851	Lactoferrin derive
38	11	47.8	3	15	AA04852	Lactoferrin derive
39	11	47.8	3	15	AA04857	Endothelin antag
40	11	47.8	3	15	AA04951	Lactoferrin derive
41	11	47.8	3	15	AA05745	Lactoferrin derive
42	11	47.8	3	15	AA05745	Lactoferrin derive
43	11	47.8	3	15	AA05745	Angiotensin I conv
44	11	47.8	3	15	AA05857	Angiotensin I conv
45	11	47.8	3	15	AA05857	Angiotensin I conv

ALIGNMENTS

RESULT 1	
AA06521	
ID	AA06521 standard; peptide; 8 AA.
XX	
AC	AA06521;
XX	
DT	28-SEP-2000 (first entry)
XX	
DE	Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
XX	
KW	Claudin-2 modulating agent; cell adhesion recognition sequence;
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW	graft rejection.
XX	
OS	Mammalia.
XX	
FN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaschuck OW, Symonds JM, Gour BJ;
XX	
DR	WPI; 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing

PT vasopermiability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 46; Page 97; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 8 AA;  
  
Query Match 60.9%; Score 14; DB 21; Length 8;  
Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 1 WRTSSYVG 8  
  
RESULT 2  
AAB06574  
ID AAB06574 standard; peptide; 8 AA.  
XX  
AC AAB06574;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.  
XX  
KW Claudin-2 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermiability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 49; Page 98; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 8 AA;

Query Match 60.9%; Score 14; DB 21; Length 8;  
Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 1 WRTSSYVG 8  
  
RESULT 3  
AAB06823  
ID AAB06823 standard; peptide; 8 AA.  
XX  
AC AAB06823;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-7 cell adhesion recognition sequence SEQ ID NO: 394.  
XX  
KW Claudin-7 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermiability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 76; Page 104; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 8 AA;  
  
Query Match 60.9%; Score 14; DB 21; Length 8;  
Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 1 WQWSSYAG 8  
  
RESULT 4  
AAB06876  
ID AAB06876 standard; peptide; 8 AA.  
XX  
AC AAB06876;  
XX

28-SEP-2000 (first entry)  
 Claudin-7 cyclic cell adhesion recognition sequence SEQ ID NO: 447.  
 Claudin-7 modulating agent; cell adhesion recognition sequence;  
 CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 graft rejection; cyclic.  
 Mammalia.  
 WO200026360-A1.  
 11-MAY-2000.  
 03-NOV-1999; 99WO-CA01029.  
 03-NOV-1998; 98US-0185908.  
 30-MAR-1999; 99US-0282029.  
 (ADHE-) ADHEREX TECHNOLOGIES INC.  
 Blaschuck OW, Symonds JM, Gour BJ;  
 WPI; 2000-365610/31.  
 Antibody modulation of claudin-mediated cell adhesion for increasing  
 vasopermeability, for delivering drugs to tumors and the nervous system  
 and across the skin -  
 Claim 79; Page 105; 121pp; English.  
 The present invention relates to the use of peptides as claudin-mediated  
 cell adhesion modulators. The claudin-7 group of proteins are cadherins,  
 which are membrane glycoproteins involved in cell adhesion. In some  
 situations, cell adhesion occurs at abnormal levels, and these peptides  
 can be used to modulate these levels, and thus treat autoimmune diseases,  
 inflammatory diseases and cancer, and aid wound healing and implant  
 adhesion. In addition, they can also be used to facilitate drug delivery  
 to the desired target site. The present sequence has a cyclic  
 conformation.

Query Match 60.9%; Score 14; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 WXXXXXXG 8  
 Db 1 WQSSSYAG 8

RESULT 5  
 AAB06917  
 ID AAB06917 standard; Protein; 8 AA.  
 AC AAB06917;  
 DT 05-OCT-2000 (first entry)  
 DE Claudin-7 cell adhesion recognition modulating sequence SEQ ID NO: 50.  
 KW Claudin-7 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site 8 /note= "N-terminal acetyl"  
 FT Modified-site 8 /note= "C-terminal amide"

XX WO200026360-A1.  
 PN 11-MAY-2000.  
 PD 03-NOV-1999; 99WO-CA01029.  
 PF 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX Blaschuck OW, Symonds JM, Gour BJ;  
 XX WPI; 2000-365610/31.  
 XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 PS Claim 77; Page 104; 121pp; English.  
 XX The present sequence is a peptide which can be used in a claudin-mediated  
 CC cell adhesion modulator. The claudin group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and this peptide  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, it can also be used to facilitate drug delivery  
 CC to the desired target site.  
 XX Sequence 8 AA;  
 SQ Query Match 60.9%; Score 14; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 WXXXXXXG 8  
 Db 1 WQSSSYAG 8

RESULT 6  
 AAB56267  
 ID AAB56267 standard; Protein; 8 AA.  
 XX AAB56267;  
 AC AAB56267;  
 DT 13-MAR-2001 (first entry)  
 DE Human secreted protein sequence encoded by gene 65 SEQ ID NO:361.  
 XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
 KW antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic;  
 KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
 KW fungicide; ophthalmological; gene therapy; pathological condition;  
 KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;  
 KW neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;  
 KW cerebrovascular disorder; angiogenesis; nervous system disorder;  
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
 KW wound healing; skin aging; food additive; preservative.  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200070042-A1.  
 XX 23-NOV-2000.  
 PD 11-MAY-2000; 2000WO-US12788.  
 PF 13-MAY-1999; 99US-0134068.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 XX

XX Roen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;  
PI Duan RD, Florence KA, Soppet DR;  
XX WPI; 2000-679828/66.  
XX Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
XX Disclosure; Page 1021; 1065pp; English.  
XX The polynucleotide sequences given in AAC99818 to AAC99977 encode the  
CC human secreted proteins given in AAB56077 to AAB56362. Human secreted  
CC proteins have activities based on the tissues and cells the genes are  
CC expressed in. Examples of activities include: immunosuppressive;  
CC antihypertensive; antirheumatic; antiproliferative; cytostatic; cardiac;  
CC vasotropic; cerebroprotective; neurotrophic; neuroprotective; antibacterial;  
CC virucide; fungicide; and ophthalmological. The human secreted  
CC polynucleotides and proteins can be used to prevent, treat or ameliorate  
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
CC dogs, chickens or sheep. They are also used in diagnosing a pathological  
CC condition or susceptibility to a pathological condition. Disorders which  
CC are diagnosed or treated include autoimmune diseases e.g. rheumatoid  
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders  
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
CC fungi and ocular disorders e.g. corneal infection. The proteins can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The proteins can also be used as a  
CC food additive or preservative to increase or decrease storage  
CC capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used  
CC in the exemplification of the present invention.  
XX Sequence 8 AA;  
XX Query Match 56.5%; Score 13; DB 21; Length 8;  
XX Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
XX Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
OY 1 WXXXXXXG 8  
DB 1 WGLVTLAG 8  
RESULT 7  
AAB06419  
ID AAB06419 standard; peptide; 8 AA.  
XX AAB06419;  
XX 28-SEP-2000 (first entry)  
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.  
XX Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX Mammalia.  
XX WO200026360-A1.  
XX 11-MAY-2000.  
XX 03-NOV-1999; 99WO-CA01029.  
XX 03-NOV-1998; 98US-0185908.  
XX 30-MAR-1999; 99US-0282029.  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX Claim 39; Page 96; 121pp; English.  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX Sequence 8 AA;  
XX Query Match 56.5%; Score 13; DB 21; Length 8;  
XX Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
XX Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
OY 1 WXXXXXXG 8  
DB 1 WKIVSYAG 8  
RESULT 8  
AAB06426  
ID AAB06426 standard; peptide; 8 AA.  
XX AAB06426;  
XX 28-SEP-2000 (first entry)  
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.  
XX Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX Mammalia.  
XX WO200026360-A1.  
XX 11-MAY-2000.  
XX 03-NOV-1999; 99WO-CA01029.  
XX 03-NOV-1998; 98US-0185908.  
XX 30-MAR-1999; 99US-0282029.  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX Claim 39; Page 96; 121pp; English.  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.

XX Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX Claim 39; Page 96; 121pp; English.  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX Sequence 8 AA;  
XX Query Match 56.5%; Score 13; DB 21; Length 8;  
XX Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
XX Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
OY 1 WXXXXXXG 8  
DB 1 WKIVSYAG 8  
RESULT 8  
AAB06426  
ID AAB06426 standard; peptide; 8 AA.  
XX AAB06426;  
XX 28-SEP-2000 (first entry)  
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.  
XX Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX Mammalia.  
XX WO200026360-A1.  
XX 11-MAY-2000.  
XX 03-NOV-1999; 99WO-CA01029.  
XX 03-NOV-1998; 98US-0185908.  
XX 30-MAR-1999; 99US-0282029.  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX Claim 39; Page 96; 121pp; English.  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,

CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site.

XX Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 |  
 Db 1 WRIYSYAG 8

# RESULT 9

AAB06479  
 ID AAB06479 standard; peptide; 8 AA.

XX AC

XX AC AAB06479;

XX 28-SEP-2000 (first entry)

XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.

XX Claudin-1 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.

XX OS Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -

XX Claim 43; Page 97; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.

XX Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 |  
 Db 1 WKIYSYAG 8

# RESULT 10

AAB06512

ID AAB06512 standard; peptide; 8 AA.

XX AC

XX AC AAB06512;

XX 28-SEP-2000 (first entry)

XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.

XX Claudin-1 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.

XX OS Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -

XX Claim 43; Page 97; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.

XX Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 |  
 Db 1 WRIYSYAG 8

# RESULT 11

AAB06583

ID AAB06583 standard; peptide; 8 AA.

XX AC

XX AC AAB06583;

XX 28-SEP-2000 (first entry)

XX Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.

XX Claudin-3 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection.

XX OS Mammalia.



SQ Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WXXXXXXG 8  
 |  
 Db 1 WRVTAFIG 8

RESULT 14

AAB06698  
ID AAB06698 standard; peptide; 8 AA.

XX AC AAB06698;

XX DT 28-SEP-2000 (first entry)

XX DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 216.

XX KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
 XX KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 XX KW graft rejection; cyclic.

XX OS Mammalia.

XX PN WO200026360-A1.

XX PD 11-MAY-2000.

XX PF 03-NOV-1999; 99WO-CA01029.

XX PR 03-NOV-1998; 98US-0185908.

XX PR 30-MAR-1999; 99US-0282029.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuck OW, Symonds JM, Gour BJ;

XX DR WPI; 2000-365610/31.

XX XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -

XX PS Claim 61; Page 101; 121pp; English.

XX CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.

SQ Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WXXXXXXG 8  
 |  
 Db 1 WRVTAFIG 8

RESULT 15

AAB06764  
ID AAB06764 standard; peptide; 8 AA.

XX

AC AAB06764;  
 XX DT 28-SEP-2000. (first entry)  
 XX DE Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.  
 XX KW Claudin-6 modulating agent; claudin-9 modulating agent;  
 KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
 KW inflammatory disease; cancer; graft rejection.  
 XX OS Mammalia.  
 XX PN WO200026360-A1.  
 XX PD 11-MAY-2000.  
 XX PF 03-NOV-1999; 99WO-CA01029.  
 XX PR 03-NOV-1998; 98US-0185908.  
 XX PR 30-MAR-1999; 99US-0282029.  
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PI Blaschuck OW, Symonds JM, Gour BJ;  
 XX DR WPI; 2000-365610/31.  
 XX XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -

XX PS Claim 70; Page 103; 121pp; English.

XX CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
 CC are cadherins, which are membrane glycoproteins involved in cell  
 CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
 CC and these peptides can be used to modulate these levels, and thus treat  
 CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
 CC healing and implant adhesion. In addition, they can also be used to  
 CC facilitate drug delivery to the desired target site.

SQ Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WXXXXXXG 8  
 |  
 Db 1 WKVTAFIG 8

Search completed: January 12, 2004, 08:22:58  
 Job time : 74 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2004, 08:20:13 ; Search time 37 Seconds  
(without alignments)  
20.793 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 604

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	47.8	3	F37196	bradykinin-potenti
2	11	47.8	4	A34626	RPCH-related neuro
3	11	47.8	4	B53284	T-cell receptor be
4	11	47.8	4	PT0661	T-cell receptor be
5	11	47.8	5	A32516	cholecystokinin-5
6	11	47.8	5	A60803	neuropeptide - sea
7	11	47.8	5	JH0253	gut pentapeptide -
8	11	47.8	5	G37196	bradykinin-potenti
9	11	47.8	5	PT0281	ig heavy chain CRD
10	11	47.8	5	PT0308	ig heavy chain CRD
11	11	47.8	5	PT0729	T-cell receptor be
12	11	47.8	5	PT0580	T-cell receptor be
13	11	47.8	6	S66195	alcohol dehydrogen
14	11	47.8	6	B34835	dnaa protein - fse
15	11	47.8	6	A31263	dihydrofolate redu
16	11	47.8	6	B31263	locustakinin - mig
17	11	47.8	6	A61068	cerebellar degener
18	11	47.8	6	B35640	T-cell receptor be
19	11	47.8	6	PT0629	T-cell receptor be
20	11	47.8	6	PT0532	T-cell receptor be
21	11	47.8	6	PT0519	T-cell receptor be
22	11	47.8	6	PT0637	T-cell receptor be
23	11	47.8	6	PT0641	T-cell receptor be
24	11	47.8	6	PT0726	T-cell receptor be
25	11	47.8	6	P41945	T-cell receptor ga
26	11	47.8	6	PT0028	pev-kinin 2 - pena
27	11	47.8	6	I79564	hypothetical TGL3
28	11	47.8	7	S21230	dermorphin (Trp-4,
29	11	47.8	7	A58512	venom heptapeptide

30	11	47.8	7	2	A61081	tryptophyllin, bas
31	11	47.8	7	2	S57274	triacylglycerol li
32	11	47.8	7	2	S09652	hypothetical prote
33	11	47.8	7	2	PQ0727	H2 class I protein
34	11	47.8	7	2	S33244	neuromodulatory pe
35	11	47.8	7	2	S33245	neuromodulatory pe
36	11	47.8	7	2	S33246	neuromodulatory pe
37	11	47.8	7	2	E48394	glycoprotein compo
38	11	47.8	7	2	PH1602	ig H chain V-D-J r
39	11	47.8	7	2	PT0526	T-cell receptor be
40	11	47.8	7	2	PT0628	T-cell receptor be
41	11	47.8	7	2	PT0642	T-cell receptor be
42	11	47.8	7	2	PT0722	T-cell receptor be
43	11	47.8	7	2	PT0688	T-cell receptor be
44	11	47.8	7	2	PT0586	T-cell receptor be
45	11	47.8	7	2	PT0728	T-cell receptor be

## ALIGNMENTS

### RESULT 1

F37196  
bradykinin-potentiating peptide 6 - island jararaca  
C:Species: Bothrops insularis (island jararaca)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
R:Accession: F37196  
R:Cintrra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A:Title: Primary structure and biological activity of bradykinin potentiating peptide:  
A:Reference number: A37196; MUID:90351557; PMID:2386615  
A:Accession: F37196  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-3 <GIN>  
C:Keywords: pyroglutamic acid  
F:1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 47.8%; Score 11; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 3 W 3

### RESULT 2

A34626  
RPCH-related neuropeptide - ferruginous spindle  
C:Species: Fusinus ferrugineus (ferruginous spindle)  
C:Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 31-Dec-1993  
R:Accession: A34626  
R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.  
Biochem. Biophys. Res. Commun. 167, 273-279, 1990  
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.  
A:Reference number: A34626; MUID:90179762; PMID:2310394  
A:Accession: A34626  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <KUR>  
C:Keywords: neuropeptide

Query Match 47.8%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 4 W 4

### RESULT 3



B53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: B53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and J  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: B53284  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-4 <HAR>  
A:Cross-references: GB:S60737; NID:9233916; PIDN:AAB19518.1; PID:9233918  
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)  
C:Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 2 W 2

RESULT 4  
PT0661  
T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0661  
R:Peeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0661  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <FES>  
A:Experimental source: day 4 postnatal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 3 W 3

RESULT 5  
A32516  
cholecystokinin-5 - dog  
N:Alternate names: CCK-5  
C:Species: Canis lupus familiaris (dog)  
C:Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C:Accession: A32516  
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.  
Am. J. Physiol. 252, G272-G275, 1987  
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest  
A:Reference number: A32516; MUID:87153871; PMID:3826354  
A:Accession: A32516  
A:Molecule type: protein  
A:Residues: 1-5 <SHI>  
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; neuropeptide  
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 2 W 2

RESULT 6  
A60803  
neuropeptide - sea anemone (Anthopleura elegantissima)  
C:Species: Anthopleura elegantissima  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: A60803  
R:Graff, D.; Grimmelikhuijzen, C.J.P.  
Brain Res. 442, 354-358, 1988  
A:Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemone  
A:Reference number: A60803; MUID:88222764; PMID:2897223  
A:Accession: A60803  
A:Molecule type: protein  
A:Residues: 1-5 <GRA>  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 5 W 5

RESULT 7  
JH0253  
gut pentapeptide - Japanese eel  
C:Species: Anguilla japonica (Japanese eel)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C:Accession: JH0253  
R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A:Reference number: JH0253; MUID:92062113; PMID:1953755  
A:Accession: JH0253  
A:Molecule type: protein  
A:Residues: 1-5 <UES>  
A:Experimental source: gut  
C:Comment: This peptide increased basal tone of the circular muscle of the esophagoga  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 3 W 3

RESULT 8  
G37196  
bradykinin-potentiating peptide 7 - island jataraca  
C:Species: Bothrops insularis (island jararaca)  
C:Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994  
C:Accession: G37196  
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A:Title: Primary structure and biological activity of bradykinin potentiating peptide  
A:Reference number: A37196; MUID:90351557; PMID:2386615  
A:Accession: G37196  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <CIN>

C;Keywords: pyroglutamic acid  
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 3 W 3

## RESULT 9

PT0281  
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0281  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0281

A;Molecule type: DNA

A;Residues: 1-5 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 4 W 4

## RESULT 10

PT0308

Ig heavy chain CRD3 region (clone 6-88) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0308

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0308

A;Molecule type: DNA

A;Residues: 1-5 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 2 W 2

## RESULT 11

PT0729

T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0640; PT0685; PT0729

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0640

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FE2>

A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J

A;Accession: PT0685

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-5 <FE2>

A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C

A;Accession: PT0729

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-5 <PE3>

A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG

C;Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 5 W 5

## RESULT 12

PT0580

T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0580

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0580

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <PE2>

A;Experimental source: day 19 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 4 W 4

## RESULT 13

S66195

alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (frag

C;Species: Gadus sp. (cod)

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 12-Jun-1998

C;Accession: S66195

R;Hjeltnes, L.; Hackett, M.; Shafiqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C

FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66195

A;Molecule type: protein

A;Residues: 1-6 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 47.8%; Score 11; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|

```

Db      |
      5 W 5

RESULT 14
B34835
dnaA protein - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C:Accession: B34835
R:Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
A:Reference number: A34835; MUID:90160310; PMID:2106132
A:Accession: B34835
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <YEE>
A:Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
C:Keywords: DNA binding

Query Match      47.8%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 W 1
      |
Db      6 W 6

RESULT 15
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Welles, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: A31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match      47.8%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 W 1
      |
Db      3 W 3

Search completed: January 12, 2004, 08:26:05
Job time : 39 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2004, 08:13:32 ; Search time 23 seconds  
(without alignments)  
16.357 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	11	47.8	4	1 OCP3 OCTMI	P58649 octopus min
2	11	47.8	5	1 BPP7 BOTIN	P30425 bothrops in
3	11	47.8	5	1 UF01 MOUSE	P38639 mus musculus
4	11	47.8	6	1 E101 LITRU	P82096 litoria rub
5	11	47.8	6	1 LOK1 LOCMI	P41491 locusta mig
6	11	47.8	7	1 BRHP CONIM	P58803 conus imper
7	11	47.8	7	1 TPY1 PACDA	P83455 pachymedusa
8	11	47.8	7	1 TPY1 LITRU	P82065 litoria rub
9	11	47.8	7	1 WWA1 ACHFU	P35919 achatina fu
10	11	47.8	7	1 WWA2 ACHFU	P35920 achatina fu
11	11	47.8	7	1 WWA3 ACHFU	P35921 achatina fu
12	11	47.8	8	1 AC1 THUAL	P18691 thunnus alb
13	11	47.8	8	1 AKHG GRYBI	P14086 gryllus bim
14	11	47.8	8	1 AKH LIBAU	P25418 libellula a
15	11	47.8	8	1 AKH MELML	P25423 melolontha
16	11	47.8	8	1 AKH TABAT	P14595 tabanus atr
17	11	47.8	8	1 CCKN MACEU	P30369 macropus eu
18	11	47.8	8	1 COM2 CONPU	P58785 conus purpu
19	11	47.8	8	1 HTP1 PERAM	P04548 periplaneta
20	11	47.8	8	1 HTP2 PERAM	P04549 periplaneta
21	11	47.8	8	1 HTP TENMO	P25419 tenebrio mo
22	11	47.8	8	1 LCK1 LEUMA	P21140 leucophaea
23	11	47.8	8	1 LCK2 LEUMA	P21141 leucophaea
24	11	47.8	8	1 LCK3 LEUMA	P21142 leucophaea
25	11	47.8	8	1 LCK4 LEUMA	P21143 leucophaea
26	11	47.8	8	1 LCK5 LEUMA	P19987 leucophaea
27	11	47.8	8	1 LCK6 LEUMA	P19988 leucophaea
28	11	47.8	8	1 LCK7 LEUMA	P19989 leucophaea
29	11	47.8	8	1 LCK8 LEUMA	P19990 leucophaea
30	11	47.8	8	1 PLP BRANA	P81707 brassica bo
31	11	47.8	8	1 RPCH PANBO	P08939 pandalus bo
32	11	47.8	8	1 RT34 BOVIN	P82929 bos taurus
33	6	26.1	3	1 GRWM HUMAN	P01157 homo sapien

34	6	26.1	4	1 ACH1 ACHFU	P35904 achatina fu
35	6	26.1	4	1 DCML PSECH	P19916 pseudomonas
36	6	26.1	4	1 E0S1 HUMAN	P02731 homo sapien
37	6	26.1	4	1 OCP1 OCTMI	P58648 octopus min
38	6	26.1	5	1 AL14 CARMA	P81817 cardinus ma
39	6	26.1	5	1 PAP2 PARMA	P81864 pardachirus
40	6	26.1	5	1 RE32 LITRU	P82073 litoria rub
41	6	26.1	5	1 TPIS CANPA	P54714 canis famil
42	6	26.1	5	1 UXA4 CHLTR	P38005 chlamydia t
43	6	26.1	6	1 CIP1 MYTED	P13736 mytilus edu
44	6	26.1	6	1 CIP2 MYTED	P13737 mytilus edu
45	6	26.1	6	1 PARP MONEX	P41966 moniezia ex

ALIGNMENTS

RESULT 1					
OCP3 OCTMI					
ID	OCP3 OCTMI	STANDARD;	PRT;	4 AA.	
AC	P58649;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DE	Cardioactive peptides Ocp-3/Ocp-4.				
OS	Octopus minor (Octopus).				
OC	Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;				
OC	Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.				
OX	NCBI_TaxID=89766;				
RN	[1]				
RP	SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.				
RC	TISSUE=Brain;				
RX	MEDLINE=20336815; PubMed=10876044;				
RA	Iwakoshi E., Hisada M., Minakata H.;				
RT	"Cardioactive peptides isolated from the brain of a Japanese octopus,				
RL	Octopus minor.";				
RL	Peptides 21:623-630(2000).				
CC	-!- FUNCTION: Cardioactive; has both positive chronotropic and				
CC	inotropic effects on the heart. Ocp-4 is a 1000 time less				
CC	active than Ocp-3.				
CC	-!- SUBCELLULAR LOCATION: Secreted.				
CC	-!- PTM: Ocp-4 has D-Ser instead of L-Ser.				
CC	-!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.				
KW	Hormone; D-amino acid.				
FT	MOD RES 2				
SQ	SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;				
Query Match					
Best Local Similarity 47.8%; Score 11; DB 1; Length 4;					
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1 W 1				
Db	3 W 3				
RESULT 2					
BPP7 BOTIN					
ID	BPP7 BOTIN	STANDARD;	PRT;	5 AA.	
AC	P30425;				
DT	01-APR-1993 (Rel. 25, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DE	Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting				
DE	enzyme inhibitor).				
OS	Bothrops insularis (Island jararaca) (Queimada jararaca).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;				
OC	Viperidae; Crotalinae; Bothrops.				
RN	NCBI_TaxID=8723;				
RP	SEQUENCE.				
RC	TISSUE=Venom;				

RA MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; G37196; G37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;  
  
Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 W 1  
DB 3 W 3  
  
RESULT 3  
UF01\_MOUSE STANDARD; PRT; 5 AA.  
AC P38639;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
RT using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.6, ITS MW IS: 19 KDa.  
FT NON TER 5 5  
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;  
  
Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 W 1  
DB 1 W 1  
  
RESULT 4  
EI01\_LITRU STANDARD; PRT; 6 AA.  
AC P82036;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyllidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Skin secretion;

RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 6 6 AMIDATION.  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;  
  
Query Match 47.8%; Score 11; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 W 1  
DB 5 W 5  
  
RESULT 5  
LOKI\_LOCM1 STANDARD; PRT; 6 AA.  
AC P41491;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Locustakinin I.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=92262851; PubMed=1585017;  
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
RA de Loof A.;  
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,  
RT isolation, primary structure and synthesis.";  
RL Regul. Pept. 37:49-57(1992).  
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation  
CC of ion transport and inhibition of diuretic activity in Malpighian  
CC tubules.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
DR PIR; A61068; A61068.  
KW Neuropeptide; Amidation.  
FT MOD RES 6 6 AMIDATION.  
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;  
  
Query Match 47.8%; Score 11; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 W 1  
DB 5 W 5  
  
RESULT 6  
BRHP\_CONIM STANDARD; PRT; 7 AA.  
AC P58803;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bromheptapeptide Im.  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;

RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RP TISSUE-Venom;  
 RC MEDLINE=97184108; PubMed=9030520;  
 RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,  
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,  
 RA McIntosh J.M.;  
 RT "A novel post-translational modification involving bromination of  
 RT tryptophan. Identification of the residue, L-6-bromotryptophan, in  
 RL J. Biol. Chem. 272:4689-4698(1997).  
 CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected  
 CC centrally or peripherally in mice.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.  
 DR PIR, A58512; A58512;  
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.  
 FT DISULFID 2 7  
 FT MOD\_RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 6 6 6 BROMINATION.  
 FT MOD\_RES 7 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;  
 Query Match 47.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 W 1  
 Db 6 W 6

RESULT 7  
 TPFY\_PACDA STANDARD; PRT; 7 AA.  
 AC P83455;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin-1 (PdT-1).  
 OS Pachymedusa dactinolor (Giant mexican leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phyllomedusinae; Pachymedusa.  
 OX NCBI\_TaxID=75988;  
 RN SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
 RP PRO-7.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Shaw C.;  
 RT "Pachymedusa dactinolor tryptophyllin-1 (PdT-1): structural  
 RT characterization, pharmacological activity and cloning of precursor  
 RT cDNA.";  
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
 CC smooth muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.  
 KW Amphibian defense peptide; Amidation; Hydroxylation.  
 FT MOD\_RES 3 3 3 HYDROXYLATION.  
 FT MOD\_RES 7 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC77676350 CRC64;  
 Query Match 47.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 W 1  
 Db 1

Db 5 W 5

RESULT 8  
 TY51\_LITRU STANDARD; PRT; 7 AA.  
 ID TY51\_LITRU  
 AC P82065;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin 5.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RP RP  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=PAB.  
 KW Amphibian defense peptide; Amidation; Neuropeptide;  
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 1 1 1  
 FT MOD\_RES 7 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;  
 Query Match 47.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 W 1  
 Db 4 W 4

RESULT 9  
 WWAL\_ACHFU STANDARD; PRT; 7 AA.  
 ID WWAL\_ACHFU  
 AC P35919;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Wwamide-1.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN SEQUENCE.  
 RP RP  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nonoto K.;  
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 RT ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108(1993).  
 CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS  
 CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.  
 DR PIR; S33245; S33245.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;  
 Query Match 47.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 1 W 1

## RESULT 10

WAA2 ACHFU  
ID WAA2 ACHFU STANDARD; PRT; 7 AA.  
AC P35920;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE WAA2 ACHFU  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylommatophora;  
OC Sigamurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN RP  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL PIR; S33246; S33246.  
DR PIR; S33246; S33246.  
KW Neuropetide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 1 W 1

## RESULT 11

WAA3 ACHFU  
ID WAA3 ACHFU STANDARD; PRT; 7 AA.  
AC P35921;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE WAA3 ACHFU  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigamurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN RP  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL PIR; S33244; S33244.  
DR PIR; S33244; S33244.  
KW Neuropetide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 1 W 1

## RESULT 12

ACI THUAL  
ID ACI THUAL STANDARD; PRT; 8 AA.  
AC P18691;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Angiotensin-converting enzyme inhibitor.  
OS Thunus albacares (Yellowfin tuna) (Neothunnus macropterus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; Thunnus.  
OX NCBI\_TaxID=8236;  
RN RP  
RP SEQUENCE.  
RC TISSUE=Muscle;  
RX MEDLINE=88326322; PubMed=3415688;  
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;  
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna  
RT muscle.";  
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).  
DR PIR; A31570; A31570.  
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 6 W 6

## RESULT 13

AKHG GRYBI  
ID AKHG GRYBI STANDARD; PRT; 8 AA.  
AC P14086;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Adipokinetic hormone G (AKH-G) (80 II).  
OS Gryllus bimaculatus (Two-spotted cricket), and  
OS Romalea microptera (lubber grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Gryllus.  
OX NCBI\_TaxID=6999, 7007;  
RN RP  
RP SEQUENCE.  
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;  
RX MEDLINE=88106553; PubMed=3426616;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary sequence analysis by fast atom bombardment mass spectrometry  
RT of a peptide with adipokinetic activity from the corpora cardiaca of  
RT the cricket Gryllus bimaculatus.";  
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).  
RN RP  
RP SEQUENCE.  
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948;  
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
RT the lubber grasshopper, Romalea microptera.";  
RL Peptides 9:681-685(1988).  
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; A28004; A28004.

DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 W 1  
Db 8 W 8

## RESULT 14

AKH\_LIBAU STANDARD; PRT; 8 AA.  
ID AKH\_LIBAU  
AC P25418;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Adipokinetic hormone (AKH)  
OS Libellula auripennis (Skimmer dragonfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.  
OX NCBI\_TaxID=6966;

[1]  
RN RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=90359055; PubMed=2390213;  
RA Gaede G.;  
RT "The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone family isolated and sequenced from a dragonfly."  
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).  
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; S10596; S10596.  
DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 W 1  
Db 8 W 8

## RESULT 15

AKH\_MELML STANDARD; PRT; 8 AA.  
ID AKH\_MELML  
AC P25423;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Adipokinetic hormone (AKH)  
OS Melolontha melolontha (Cockchafer).  
OS Geotrupes stercorarius (Dor beetle), and  
OS Pachnoda marginata (flower beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;  
OC Scarabaeidae; Melolonthinae; Melolontha.

OX NCBI\_TaxID=7061, 7087, 7058;  
RN [1]  
RN SEQUENCE.  
RC SPECIES=M.melolontha, and G.stercorarius; TISSUE=Corpora cardiaca;  
RX MEDLINE=91248100; PubMed=2039445;  
RA Gaede G.;  
RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."  
RL Biochem. J. 275:671-677(1991).  
RN [2]

RN RP SEQUENCE.  
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;  
RX MEDLINE=92265187; PubMed=1586453;  
RA Gaede G., Lopata A., Keilner R., Rinehart K.L. Jr.;  
RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry."  
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).  
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; A58641; A58641.  
DR PIR; S15422; S15422.  
DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 W 1  
Db 8 W 8

Search completed: January 12, 2004, 08:23:36  
Job time : 25 secs



> O <  
O| |O IntelliGenetics  
> O <

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "seq1-iss" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence.

Selected sequence key from "new.key".

seq1 (AA) ID seq1 AA preliminary pattern

1 followed by  
2 w  
2 k or x  
2 any character  
2 any character  
2 s or a  
2 y or f  
2 any character  
2 g

Selected data banks and files:

Data bank : Issued\_AA , all entries

-- Output Parameters --

Format Options:  
Nucleic acid code matching Exact Indirect file  
Find non-matching hits only No Sequence or key file  
Report key used Yes List of hits  
Note position of hit Yes Hit display  
Display full annotations Yes Name and annotations  
Sequence context 50

-- Run Parameters --

Run mode Batch  
Time to start comparison now  
Notify at end of run No

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1 match found in sequence:  
US-08-608-241-2 ; Sequence 2, Application US/08608241  
(from "/arch/iaa/5A.COMB.pep")  
Sequence 2, Application US/08608241  
Patent No. 5747328  
GENERAL INFORMATION:  
APPLICANT: Donohue, Timothy J  
APPLICANT: Barber, Robert D  
APPLICANT: Witthuhn, Vernon  
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE  
TITLE OF INVENTION: SENSING AND REMEDIATION  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/608,241  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 960296.93511  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
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266 YTFDCTGNVQVMRQALEACHRGWGQSIIVGVAPAGABIQTRPFQLVTRGVWKGSAFGAR 316 323  
326 GRTDVPKIVDWMYEGKIQIDPMITHILSLSEINKGFDLMHAGESIRSV  
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1 match found in sequence:  
US-08-922-182-2 ; Sequence 2, Application US/08922182  
(from "/arch/iaa/5B.COMB.pep")  
Sequence 2, Application US/08922182  
Patent No. 5834300  
GENERAL INFORMATION:  
APPLICANT: Donohue, Timothy J  
APPLICANT: Barber, Robert D  
APPLICANT: Witthuhn, Vernon  
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE  
TITLE OF INVENTION: SENSING AND REMEDIATION  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/922,182  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/608,241  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 960296.93511  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
Found using 'seq1' (new.key)  
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316 323

326 GRTDVPKIVDWMYMEGKIQIDPMITHILSLBEINKGFDLMHAGESIRSV

1 match found in sequence:  
US-08-919-953-2 ; Sequence 2, Application US/08919953  
(from "/arch/iaa/5B COMB.pep")  
Sequence 2, Application US/08919953  
Patent No. 5817481

GENERAL INFORMATION:  
APPLICANT: Donohue, Timothy J  
APPLICANT: Barber, Robert D  
APPLICANT: Witthuhn, Vernon  
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE  
TITLE OF INVENTION: SENSING AND REMEDIATION  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US

ZIP: 53703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,953  
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/608,241

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 960296.93511

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Found using 'seql' (new.key)

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326 GRTDVPKIVDWMYMEGKIQIDPMITHILSLBEINKGFDLMHAGESIRSV

1 match found in sequence:  
US-08-637-759B-89 ; Sequence 89, Application US/08637759B  
(from "/arch/iaa/5B COMB.pep")  
Sequence 89, Application US/08637759B  
Patent No. 5876931  
GENERAL INFORMATION:

APPLICANT: David William Holden  
TITLE OF INVENTION: Identification of Genes  
NUMBER OF SEQUENCES: 501  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,759B

FILING DATE: 03-MAY-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/02875

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: RPMS 101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8794

TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 759 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

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1 NYTHGRILLCQILKQTFLEDELLFKALANWKPAQFGIPQRLFLRLDGLAMSCSPPLSSS  
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61 AELWLRLHHRQIKFKXGVAMRSLWEGEV

1 match found in sequence:  
US-08-871-355A-89 ; Sequence 89, Application US/08871355A  
(from "/arch/iaa/6A COMB.pep")  
Sequence 89, Application US/08871355A  
Patent No. 6015669  
GENERAL INFORMATION:

APPLICANT: David William Holden

TITLE OF INVENTION: Identification of Genes

NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,355A  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/02875  
FILING DATE: 11-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPLMS 101 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 759 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
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1 NYHNGRILLCQILKQTFLEDELLFKALANWKPAAFGIPQRLFLLRDGLAMSCSPPLSSS  
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US-09-222-817-2 ; Sequence 2, Application US/09222817  
(from "/arch/iaa/6A.COMB.pep")  
Sequence 2, Application US/09222817  
Patent No. 6037154  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP813  
CURRENT APPLICATION NUMBER: US/09/222,817  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353521  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
Found using 'seq1' (new.key)

82 VDI PAATEAGVMVANAPTSNIHSAEHAISLLSTARQIPAAATLREGEWKRSFNGVE  
132 139

142 IFGKTVGIVGFHIGQLFAQRLAAAFETTIVAYDPYANPARAAQLNVEL

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1 match found in sequence:  
US-09-222-817-12 ; Sequence 12, Application US/09222817  
(from "/arch/iaa/6A.COMB.pep")  
Sequence 12, Application US/09222817  
Patent No. 6037154  
GENERAL INFORMATION:  
APPLICANT: Donohue, Timothy  
APPLICANT: Barber, Robert  
APPLICANT: Witthuhn, Vernon  
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and  
Remediation

APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP813  
CURRENT APPLICATION NUMBER: US/09/222,817  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353521  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Brevibacterium flavum  
Found using 'seq1' (new.key)

...

82 VDI PAATEAGVMVANAPTSNIHSAEHAISLLSTARQIPAAATLREGEWKRSFNGVE  
132 139

142 IFGKTVGIVGFHIGQLFAQRLAAAFETTIVAYDPYANPARAAQLNVEL

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1 match found in sequence:  
US-09-222-817-14 ; Sequence 14, Application US/09222817  
(from "/arch/iaa/6A.COMB.pep")  
Sequence 14, Application US/09222817  
Patent No. 6037154  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP813  
CURRENT APPLICATION NUMBER: US/09/222,817  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353521  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Brevibacterium flavum  
Found using 'seq1' (new.key)

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82 VDI PAATEAGVMVANAPTSNIHSAEHAISLLSTARQIPAAATLREGEWKRSFNGVE  
132 139

142 IFGKTVGIVGFHIGQLFAQRLAAAFETTIVAYDPYANPARAAQLNVEL

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1 match found in sequence:  
US-09-192-983-2 ; Sequence 2, Application US/09192983A  
(from "/arch/iaa/6A.COMB.pep")  
Sequence 2, Application US/09192983A  
Patent No. 6242244  
GENERAL INFORMATION:  
APPLICANT: Donohue, Timothy  
APPLICANT: Barber, Robert  
APPLICANT: Witthuhn, Vernon  
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and  
Remediation

FILE REFERENCE: 960296.95505  
CURRENT APPLICATION NUMBER: US/09/192,983A  
CURRENT FILING DATE: 1998-11-16  
EARLIER APPLICATION NUMBER: 08/919,953  
EARLIER FILING DATE: 1997-08-29  
EARLIER APPLICATION NUMBER: 08/608,241  
EARLIER FILING DATE: 1996-02-28  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 376  
TYPE: PRT  
ORGANISM: Rhodobacter sphaeroides  
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266 YTFDCTGNVKVMRQALEACHRGWGQSIIVGAPAGABIQTRPQLVTGRVWKGSAFGGAR 316  
323

326 GRTDVPKIVDWMYMEGKIQIDPMITHLSLEINKGFDLMHAGESIRSV

1 match found in sequence:  
US-09-222-786-2 ; Sequence 2, Application US/09222786A  
(from "/arch/iaa/6A COMB.pep")  
Sequence 2, Application US/09222786A  
Patent No. 6258573  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP812  
CURRENT APPLICATION NUMBER: US/09/222,786A  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353513  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
Found using 'seq1' (new.key)  
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82 VDIPATEAGVMVANAPTNIHSACEHAISLLSTARQIPAADATLREGWKRSFNGVE 132  
139

142 IFGKTVGIVGFHIGQLFAQLAFAFTTIVAYDPYANPARAAQLNVEL

1 match found in sequence:  
US-09-222-786-12 ; Sequence 12, Application US/09222786A  
(from "/arch/iaa/6A COMB.pep")  
Sequence 12, Application US/09222786A  
Patent No. 6258573  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP812  
CURRENT APPLICATION NUMBER: US/09/222,786A  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12

EARLIER APPLICATION NUMBER: JP 10-353513  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Brevibacterium flavum  
Found using 'seq1' (new.key)  
...  
82 VDIPATEAGVMVANAPTNIHSACEHAISLLSTARQIPAADATLREGWKRSFNGVE 132  
139

142 IFGKTVGIVGFHIGQLFAQLAFAFTTIVAYDPYANPARAAQLNVEL

1 match found in sequence:  
US-09-222-786-14 ; Sequence 14, Application US/09222786A  
(from "/arch/iaa/6A COMB.pep")  
Sequence 14, Application US/09222786A  
Patent No. 6258573  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP812  
CURRENT APPLICATION NUMBER: US/09/222,786A  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353513  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Brevibacterium flavum  
Found using 'seq1' (new.key)  
...  
82 VDIPATEAGVMVANAPTNIHSACEHAISLLSTARQIPAADATLREGWKRSFNGVE 132  
139

142 IFGKTVGIVGFHIGQLFAQLAFAFTTIVAYDPYANPARAAQLNVEL

1 match found in sequence:  
US-09-516-143A-2 ; Sequence 2, Application US/09516143A  
(from "/arch/iaa/6B COMB.pep")  
Sequence 2, Application US/09516143A  
Patent No. 6333182  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Human Glycosylation Enzymes  
FILE REFERENCE: PF505PCT  
CURRENT APPLICATION NUMBER: US/09/516,143A  
CURRENT FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/122,409  
PRIOR FILING DATE: 1999-03-02  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 434  
TYPE: PRT

```
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: 133
OTHER INFORMATION: Xaa equals Tyr or His
NAME/KEY: SITE
LOCATION: 136
OTHER INFORMATION: Xaa equals Gly or Val
NAME/KEY: SITE
LOCATION: 147
OTHER INFORMATION: Xaa equals Ser or Pro
NAME/KEY: SITE
LOCATION: 169
OTHER INFORMATION: Xaa equals Gly or Val
Found using 'seq1' (new.key)

...

315 KKGIEVRLISRACSKOTLSSKLCKRMEVSVSKLAVVDEWRKEMGLCWKEVAYLGN
365 372
-----|
1 NYHNGRILLCOILKQTLDEBLLFKALANWKPAAFQGIQORFLIRDLGLAMSCSPPLSSS
30 37

61 AELWLRLHHRQIKFXGVAMRSLGEGV

...

1 match found in sequence:
US-09-347-878-54 ; Sequence 54, Application US/09347878C
(from "/srch/iaa/6B-COMB.pep")
Sequence 54, Application US/09347878C
Patent No. 6376210
GENERAL INFORMATION:
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
Found using 'seq1' (new.key)

...

264 YSFCIGNVKVMRAALEACHKRGVSVVVGVAASGEIATRPFLQVTRTKGTAFGGMK
314 321
-----|
324 SVESVPLVSEYMSKKIKVDFVTHNLSFDEINKAFELMHSGKSIRTV

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1 match found in sequence:
US-09-324-541-11 ; Sequence 11, Application US/09324541
(from "/srch/iaa/6B-COMB.pep")
Sequence 11, Application US/09324541
Patent No. 6391855
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
FILE REFERENCE: 100086.412
CURRENT APPLICATION NUMBER: US/09/324,541
CURRENT FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fab fragment directed against claudin cell
TELECOMMUNICATION INFORMATION: adhesion recognition sequence
Found using 'seq1' (new.key)

1 WKIYSYAG
1 8
-----|

1 match found in sequence:
US-09-130-491-4 ; Sequence 4, Application US/09130491
(from "/srch/iaa/6B-COMB.pep")
Sequence 4, Application US/09130491
```

Patent No. 6416974  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodearl, Andrew D.J.  
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
FILE REFERENCE: 09404/041001  
CURRENT APPLICATION NUMBER: US/09/130,491  
CURRENT FILING DATE: 1998-08-07  
EARLIER APPLICATION NUMBER: US 60/058,108  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: US 60/054,961  
EARLIER FILING DATE: 1997-08-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 211  
TYPE: PRT  
ORGANISM: Homo sapiens  
Found using 'seq1' (new.key)

1 MANAGLQLGFLAFILGWIGAVSTALPQWRIYSYAGDNIVTAQMYEGLWMSCVSQSTG  
30 37  
-----|-----|  
61 QIQCKVFDLLNLSTLOATRALMVVG  
....

1 match found in sequence:  
US-09-130-491-15 ; Sequence 15, Application US/09130491  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 15, Application US/09130491  
Patent No. 6416974  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodearl, Andrew D.J.  
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
FILE REFERENCE: 09404/041001  
CURRENT APPLICATION NUMBER: US/09/130,491  
CURRENT FILING DATE: 1998-08-07  
EARLIER APPLICATION NUMBER: US 60/058,108  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: US 60/054,961  
EARLIER FILING DATE: 1997-08-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Homo sapiens  
Found using 'seq1' (new.key)

1 MMSLEITGTSIAVLGWLCTIVCCALPMWRVSAPIGSSIIITAITWEGLMNVCVQSTGM  
29 36  
-----|-----|  
61 QCKWYDLSLLALPDQLQARALIVSI  
....

1 match found in sequence:  
US-09-724-623-110 ; Sequence 110, Application US/09724623  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 110, Application US/09724623  
Patent No. 6476209  
GENERAL INFORMATION:  
APPLICANT: Glenn, Matthew  
APPLICANT: Lubbers, Mark W  
APPLICANT: Dekker, James  
TITLE OF INVENTION: Polynucleotides, materials incorporating  
TITLE OF INVENTION: them, and methods for using them.

FILE REFERENCE: 1048UI  
CURRENT APPLICATION NUMBER: US/09/724,623  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 110  
LENGTH: 306  
TYPE: PRT  
ORGANISM: Lactobacillus rhamnosus  
Found using 'seq1' (new.key)

129 PSFNLPQGMCPCTCOGLGYVDDIDVSKLIDPNKSLNQEAITFVSFGPDTWRWRRYAYSGLF  
179 186  
-----|-----|

189 DNDKPLRDYTPBEMKLLLYAPQOTLKHPAKWPRALYEGVVPRKRS  
....

1 match found in sequence:  
US-08-976-063E-8 ; Sequence 8, Application US/08976063E  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 8, Application US/08976063E  
Patent No. 6524831  
GENERAL INFORMATION:  
APPLICANT: Steinbuechel, Alexander  
APPLICANT: Priefert, Horst  
TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL  
TITLE OF INVENTION: ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND  
TITLE OF INVENTION: VANILLIC ACID AND THEIR USE  
FILE REFERENCE: Bayer-9998-CAO  
CURRENT APPLICATION NUMBER: US/08/976,063E  
CURRENT FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 196 49 655.1 GERMANY  
PRIOR FILING DATE: 1996-11-29  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 372  
TYPE: PRT  
ORGANISM: not required under old rule  
Found using 'seq1' (new.key)

260 YSFCIGNVRLMRAALECCHKWGESVIIGVAPAGAEINTRPFHLVTRGVRWGSAGGVK  
310 317  
-----|-----|

320 GRTELPSYVEKAQCGEIPLDITFIHTMGLDDINTAFDLMDEGKSIRSV  
....

1 match found in sequence:  
US-09-205-258-344 ; Sequence 344, Application US/09205258  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 344, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921

EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 344  
LENGTH: 202  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (202)  
OTHER INFORMATION: xaa equals stop translation  
Found using 'seq1' (new key)

1 MGIALAVLGWLAVMCCALPMWRVTAFIGSNIVTSQTIWEGWMMNCVVQSTGQMCKKYD  
22 29  
61 SLLALPDQLQAAALVIIS  
...

-----  
1 match found in sequence:  
US-09-205-258-463 ; Sequence 463, Application US/09205258  
(from "/srcch/iaa/6B COMB.pep")  
Sequence 463, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
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EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06





FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21227  
LENGTH: 399  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

...

289 YSFECVGNVQLMRAALECCKGWESVIIGVAGAGOEISTRPQLVTGRVWGSAGGYR 339 346

349 GRSELPYVEKAQGEIPLDTFTTHMGLEDINEAPFLMHGKSIRTV

1 match found in sequence:  
US-09-252-991A-22187 ; Sequence 22187, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 22187, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 22187  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (699)  
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
Found using 'seq1' (new.key)

1 SRRAPALSRIIRTVRTARGGPQWIRPAPFGAACRGLPGRHRRGAGRLVSPGARR 27 34

61 SRQRPAGTSGAGEYGSGLLPAR

1 match found in sequence:  
US-09-252-991A-25507 ; Sequence 25507, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 25507, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 25507  
LENGTH: 447  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

...

23 OPDGPSTKRSAGSTSKLRWVARTTRRVYSLTPTSTASRASAGSVEGWREAAFIGVS 73 80

83 TPLQRRVLEBIVLPGRLVADRTDPVEKLQRIGVLRDRAELHLRIG

1 match found in sequence:  
US-09-252-991A-25705 ; Sequence 25705, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 25705, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 25705  
LENGTH: 547  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

414 SLLPFVHGAPPADWRRYIAIEYDVAFOAPARERLGRPTIDACRMYMVRSERWKYIAYDGFR 464 471

474 AQLPDLASDPGELRDLCNDPAHAHVREAHAGMLFDWLRLGLKRTTIS

1 match found in sequence:  
US-09-252-991A-29231 ; Sequence 29231, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 29231, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29231  
LENGTH: 426  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

66 PAFRGQPVQRBSAGTAGDSDGSPSRTRLPEAIHPGRKKARLKPPRWRSAAPDGS  
116 123

126 GRLEGAAAPLVAVLARSDAEVAVGAGEMRPGRETAGQADLDRLAG

1 match found in sequence:  
US-09-328-352-5472 ; Sequence 5472, Application US/09328352  
(from "/arch/iaa/6B COMB.pep")  
Sequence 5472, Application US/09328352  
Patent No. 6562958

GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
(from "/arch/iaa/6B COMB.pep")  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5472  
LENGTH: 192  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
Found using 'seq1' (new.key)

35 NIKADLLNAEDLTSSGILIQYDGLWGSPTYLGVSCKLKQLMDATGFLWKXQSPKGL  
85 92

95 AGFTVSSLPAGDKQSTLIIIFTQCMQHGMLWGNPILPEOHQGVAYT

1 match found in sequence:  
US-09-663-600A-92 ; Sequence 92, Application US/09663600A  
(from "/arch/iaa/6B COMB.pep")  
Sequence 92, Application US/09663600A  
Patent No. 6573068

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273

PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 92  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -24...-1  
NAME/KEY: UNSURE  
LOCATION: 54,79  
OTHER INFORMATION: Xaa = any one of the twenty amino acids  
Found using 'seq1' (new.key)

1 MASLGLQLVGYIILGLLGLTLVAMLLPSWKTSYVVGASIVTAVGFSKGLMMECATHTSG  
30 37

61 ITQCDIYSTLLGLLPADIQAQAMMVT

1 match found in sequence:  
US-09-663-600A-186 ; Sequence 186, Application US/09663600A  
(from "/arch/iaa/6B COMB.pep")  
Sequence 186, Application US/09663600A  
Patent No. 6573068

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273  
PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 186  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -24...-1  
Found using 'seq1' (new.key)

1 MASLGLQLVGYIILGLLGLTLVAMLLPSWKTSYVVGASIVTAVGFSKGLMMECATHTSG  
30 37

61 ITQCDIYSTLLGLLPADIQAQAMMVT

1 match found in sequence:  
US-09-732-210-332 ; Sequence 332, Application US/09732210

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(from "/srch/iaa/6B_COMB.pep")
Sequence 332, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 332
LENGTH: 70
TYPE: PRT
ORGANISM: Methanococcus jannaschii
Found using 'seq1' (new.key)

1  MPEWRTCSFCGYEIBPGKGMVVEKDTGLVYFCSSKCEKSYRMGRNPKLKWTKVYQDMK
  4  11
61  A
...

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1 match found in sequence:
US-09-107-532A-7233 ; Sequence 7233, Application US/09107532A
(from "/srch/iaa/6B_COMB.pep")
Sequence 7233, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bueh
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7307:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
MOLECULE TYPE: linear
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...68
SEQUENCE DESCRIPTION: SEQ ID NO: 7307:
Found using 'seq1' (new.key)

1  IIKLGRRMKMKLFTGVSALLLGTILACGSGSKDQAEASNSDTLQMYQIGDKPDNF
  12  19
61  DQLMEVANK
...

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1 match found in sequence:
US-09-107-532A-7307 ; Sequence 7307, Application US/09107532A
(from "/srch/iaa/6B_COMB.pep")
Sequence 7307, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bueh
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7307:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
MOLECULE TYPE: linear
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...68
SEQUENCE DESCRIPTION: SEQ ID NO: 7307:
Found using 'seq1' (new.key)
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Number of sequence hits saved: 0

6 HPIEENKRYSAKQRQSVKRLTRECNSKADRRKLVILKKSTHNNRKLWKRYSYIGRI 56  
-----|

66 RIS 63

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1 match found in sequence:  
US-09-215-418-2 ; Sequence 2, Application US/09215418  
(from "arch/iaa/6B COMB.pep")  
Sequence 2, Application US/09215418  
Patent No. 6586217  
GENERAL INFORMATION:  
APPLICANT: Guimaraes, M. Jorge  
APPLICANT: Bazan, J. Fernando  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN SELENOPHOSPHATE SYNTHETASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/215,418  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/406,359  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0493  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
Found using 'seq1' (new.key)

2 AAAAAAGSGETWAALVAEAGSLGACWSAGRSFNSYRPFEPQTLGFSPSMRLTSPSGMK 52  
-----|

62 GCGCKVPQETLLKLEGLTRPALQPLTSLGLVGQGETVQEGGLSTRP 59

-- Search Statistics --

Times: CPU 00:01:33.10 Total Elapsed 00:01:41.00

Number of sequences searched: 328807  
Number of sequence hits: 36  
Number of separate matches: 36

! FINDPATTERNS on pir:\* allowing 0 mismatches

1 W(K,R)XX(S,A)(Y,F)XG January 12, 2004 10:19 ..  
DEHUC2 ck: 9148 len: 374 | alcohol dehydrogenase (EC 1.1.1.1) 5 [valid  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
314: VTGRT WKGTAFGG WKSVE  
A33419 ck: 6584 len: 373 | alcohol dehydrogenase (EC 1.1.1.1) class II  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
313: VTGRT WKGTAFGG WKSVE  
DERTA ck: 6609 len: 373 | alcohol dehydrogenase (EC 1.1.1.1) 2 - rat  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
313: VTGRT WKGTAFGG WKSVE  
A56643 ck: 1156 len: 374 | alcohol dehydrogenase (EC 1.1.1.1) 2 - mouse  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
314: VTGRT WKGTAFGG WKSVE  
S68061 ck: 5507 len: 373 | alcohol dehydrogenase (EC 1.1.1.1) class II  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
313: VTGRT WKGTAFGG WKSVE  
JC4967 ck: 6805 len: 376 | alcohol dehydrogenase (EC 1.1.1.1) class II  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
316: VTGRT WKGTAFGG WKSVE  
S51187 ck: 4299 len: 376 | alcohol dehydrogenase (EC 1.1.1.1) class II  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
316: VTGRT WKGTAFGG WKSVE  
A49662 ck: 6276 len: 378 | alcohol dehydrogenase (EC 1.1.1.1) class II  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
316: VTGRT WKGTAFGG FKSRD  
S51357 ck: 1032 len: 379 | alcohol dehydrogenase (EC 1.1.1.1) Fdh - fr  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
319: VVGRV WKGSAPGG WRSVS  
S71244 ck: 5257 len: 379 | alcohol dehydrogenase (EC 1.1.1.1) class II  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
317: VTGRT WKGTAFGG FKSRD

D64763 ck: 7661 len: 369 | alcohol dehydrogenase (EC 1.1.1.1) C - Esc  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
309: VTGRV WKGSAPGG VKGRS  
S57525 ck: 7402 len: 369 | alcohol dehydrogenase (EC 1.1.1.1) C - Esc  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
309: VTGRV WKGSAPGG VKGRT  
H64052 ck: 2043 len: 378 | alcohol dehydrogenase (EC 1.1.1.1) HI0185 -  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
318: VTGRV WKGSAPGG VKGRS  
S31140 ck: 583 len: 386 | alcohol dehydrogenase (EC 1.1.1.1) SFA1 -  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
322: VTGRV WKGSAPGG IKGRS  
JN0447 ck: 8341 len: 381 | alcohol dehydrogenase (EC 1.1.1.1) PDH1 -  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
320: VTGRT WKGAAPGG VKGRS  
B54075 ck: 7421 len: 663 | arachidonate 12-lipoxygenase (EC 1.13.11.3)  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
223: RVRNS WKEDAPGG YQFLN  
S30051 ck: 6102 len: 663 | arachidonate 12-lipoxygenase (EC 1.13.11.3)  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
223: RVRNS WKEDAPGG YQFLN  
I38344 ck: 431 len: 26,926 | titin, cardiac muscle [validated] - human  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(Y)XG  
18,126: NVTIK WKGPAYDG GSKIT  
NCECX5 ck: 1854 len: 1,180 | exodeoxyribonuclease V (EC 3.1.11.5) 135K c  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
901: LPGDN WRVTSYSG LQORG  
A35742 ck: 2790 len: 513 | aqualysin (EC 3.4.21.-) I precursor - Ther  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
495: AGIYL WRIYAYSG SGMYE  
S33643 ck: 8565 len: 733 | transforming protein B-myb - African clawed



S20901 ck: 1434 len: 6,805 | titin - rabbit (fragment)  
1 W(K,R)XX(S,A)(Y,F)XG  
6,485: NVTLK WKKPAVDG GSKIT

E91088 ck: 2018 len: 1,180 | DNA helicase RecB [imported] - Escherichia  
1 W(K,R)XX(S,A)(Y,F)XG  
901: LPGDN WVRTSYSG LQORG

B82091 ck: 9551 len: 1,208 | exodeoxyribonuclease V, 135 kDa chain VC232  
1 W(K,R)XX(S,A)(Y,F)XG  
906: AIDRR WVRTSYSG LVMQS

G85933 ck: 2018 len: 1,180 | DNA helicase RecB [imported] - Escherichia  
1 W(K,R)XX(S,A)(Y,F)XG  
901: LPGDN WVRTSYSG LQORG

AD0125 ck: 4557 len: 1,220 | exodeoxyribonuclease V (EC 3.1.11.5) beta d  
1 W(K,R)XX(S,A)(Y,F)XG  
904: KQODY WVRTSYSG LQORG

AB0865 ck: 4255 len: 1,181 | exonuclease V chain [imported] - Salmonella  
1 W(K,R)XX(S,A)(Y,F)XG  
901: LLYDS WVRTSYSG LQORG

T16557 ck: 2841 len: 551 | hypothetical protein K04E7.3 - Caenorhabditis  
1 W(K,R)XX(S,A)(Y,F)XG  
376: RADYS WRN1SYSG SSDCY

S41178 ck: 957 len: 159 | gene 36 protein - phage SPPI  
1 W(K,R)XX(S,A)(Y,F)XG  
77: GVSQS WRTGAFEG QDGKR

H64449 ck: 6435 len: 70 | ribosomal protein L24E - Methanococcus jann  
1 W(K,R)XX(S,A)(Y,F)XG  
4: MPE WRTCSFCG YEIEP

S23164 ck: 5378 len: 65 | light-harvesting protein alpha chain - Ectocarpus  
1 W(K,R)XX(S,A)(Y,F)XG  
58: ENPGI WKRTSYDG

A9285 ck: 5165 len: 422 | hypothetical protein nodC-like [imported]  
1 W(K,R)XX(S,A)(Y,F)XG

415: YGVSE W(R)XX(S)(Y)XG  
WRGSSYLG

D70475 ck: 5280 len: 392 | conserved hypothetical protein aq\_2044 - Agrobacterium  
1 W(K,R)XX(S,A)(Y,F)XG  
127: YVSYN WKRRSPEG KDFED

E72167 ck: 405 len: 146 | A32L protein - variola minor virus (strain  
1 W(K,R)XX(S,A)(Y,F)XG  
73: DVKQK WRCVAYPG NGFVS

JQ1834 ck: 405 len: 146 | 3L protein - variola major virus  
1 W(K,R)XX(S,A)(Y,F)XG  
73: DVKQK WRCVAYPG NGFVS

S46858 ck: 405 len: 146 | A31L protein - variola virus  
1 W(K,R)XX(S,A)(Y,F)XG  
73: DVKQK WRCVAYPG NGFVS

H90733 ck: 8757 len: 199 | probable tail assembly protein [imported] -  
1 W(K,R)XX(S,A)(Y,F)XG  
180: WRHRA WRASFTG ICNDL

F90834 ck: 2142 len: 247 | tail assembly protein [imported] - Escherichia  
1 W(K,R)XX(S,A)(Y,F)XG  
228: WRHRA WRASFTG ICNDL

B85584 ck: 3865 len: 224 | probable tail component of prophage CP-933K  
1 W(K,R)XX(S,A)(Y,F)XG  
205: WRHRA WRASFTG ICNDL

A98950 ck: 7492 len: 261 | hypothetical protein ECs2569 [imported] - E. coli  
1 W(K,R)XX(S,A)(Y,F)XG  
28: GSFVV WRMSYFG DTLAH

F82120 ck: 3098 len: 260 | zinc ABC transporter, permease protein VC20  
1 W(K,R)XX(S,A)(Y,F)XG  
28: GSFVV WRMSYFG DTLAH

F82959 ck: 5958 len: 262 | permease of ABC zinc transporter ZnuB PAS50  
1 W(K,R)XX(S,A)(Y,F)XG  
28: GSFVV WRMSYFG DTLSH

1	A64066	ck: 1426	len: 261	! probable membrane protein HI0407 - Haemophilus	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRKWAYFG	DTLSH	1	275: GMAVG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRKDAFFG	RAALL	
1	28: GVFVV										
1	E85798	ck: 7492	len: 261	! hypothetical protein yebI [imported] - Escherichia	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRRMSYFG	DTLAH	1	T44888	ck: 3832	len: 367	! probable aminomethyltransferase (EC 2.1.2.3)
1	28: GSFVV							263: GWAIG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRKDAFLG	RDALL	
1	AC0251	ck: 7586	len: 261	! high-affinity zinc uptake system membrane protein	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRRMSYFG	DTLAH	1	A39484	ck: 2015	len: 280	! androgen-withdrawal apoptosis protein RVPI1
1	28: GSFVV							29: CALPM	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRVSAFIG	SSIIT	
1	AF3531	ck: 8470	len: 284	! high-affinity zinc uptake system membrane protein	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRRWAYFG	DTMAH	1	T32510	ck: 5742	len: 246	! hypothetical protein C44B12.3 - Caenorhabditis
1	40: GCFII							87: VVKMT	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WKQSYDYG	VLAFF	
1	C64948	ck: 7831	len: 261	! probable membrane protein yebI - Escherichia	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRRMSYFG	DTLAH	1	T00479	ck: 1756	len: 303	! probable phosphatidylinositol-glycan synthase
1	28: GSFVV							15: IPGPK	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRKVAYGG	MQIGY	
1	AF2763	ck: 9687	len: 272	! hypothetical protein znuB [imported] - Agrobacterium	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRRWAYFG	DTMAH	1	A56152	ck: 5845	len: 213	! major 25k outer membrane protein precursor
1	29: GCFVV							74: IKPDD	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WKAGAFAG	WNFOQ	
1	AI0742	ck: 7341	len: 261	! high-affinity zinc uptake system membrane protein	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRRMSYFG	DTLAH	1	AC3408	ck: 5809	len: 213	! 25K outer-membrane immunogenic protein precursor
1	28: GSFVV							74: IKPDD	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WKAGAFAG	WNFOQ	
1	E97544	ck: 5850	len: 298	! permease of ABC zinc transporter znuB (PASS)	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRRWAYFG	DTMAH	1	G85506	ck: 391	len: 198	! hypothetical protein 20246 [imported] - Escherichia
1	55: GCFVV							48: VTPPQ	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRNKAFIG	LKDPE	
1	S65290	ck: 8779	len: 475	! clathrin-associated protein complex medium	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WKIRSFPG	GKEYS	1	F90655	ck: 6047	len: 215	! hypothetical protein ECs0214 [imported] - Escherichia
1	382: KSAIL							65: VTPPQ	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRNKAFIG	LKDPE	
1	C96633	ck: 2687	len: 428	! probable Serine/Threonine protein kinase P8	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WKIKSFPG	NKEYM	1	G90978	ck: 8152	len: 227	! hypothetical protein ECs2799 [imported] - Escherichia
1	346: KDALV							35: DEIKY	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRYTSYKG	GKLPE	
1	D70786	ck: 6149	len: 379	! probable gcvT protein - Mycobacterium tuberculosis	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WKIKSFPG	NKEYM	1	AF0118	ck: 8384	len: 765	! probable kinase YPO0966 [imported] - Yersinia
1								306: ADAPL	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTISYFG	GKGVV	



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1 AG0179 ck: 7342 len: 766 ! hypothetical protein YP01473 [imported] - Y
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
306: ADAPL WRTISYPG GKGVV
1 AG0697 ck: 4455 len: 122 ! probable pathogenicity island protein STY14
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
70: KALAN WKPAAFQG IPQRL
1 F87390 ck: 9243 len: 613 ! TonB-dependent receptor, probable [imported]
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(Y)XG
370: KGDTH WRAAYAG FRPPT
1 S60618 ck: 760 len: 441 ! 4-alpha-glucanotransferase (EC 2.4.1.25) -
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(Y)XG
348: EGQTF WKWPAYNG PPSGI
1 F83354 ck: 8784 len: 538 ! probable sulfatase PA2333 [imported] - Pseu
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(Y)XG
455: VRSER WKYIAYDG FRAQL
1 S78561 ck: 548 len: 937 ! CS3 pilin synthesis protein, 104K - Bacheri
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
595: SIETD WGRAPFG YLSPY
1 H75258 ck: 3668 len: 206 ! probable 3-demethylubiquinone-9 3-methyltra
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
111: VEETG WRTASPDG VVGA
1 T34972 ck: 1160 len: 330 ! probable membrane protein - Streptomyces co
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
31: KARLR WRLAPAG FVGVV
1 T06088 ck: 7947 len: 700 ! hypothetical protein T9A14.170 - Arabidopsi
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
645: PQQIN WRPPSYFG RDDLE
1 T02995 ck: 2338 len: 530 ! unspecific monooxygenase (EC 1.14.14.1) - c
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
254: RGCSP WRDPAPVG GNDYY
1 T00208 ck: 8858 len: 777 ! transposase-like protein - fungus (Fusarium
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1 W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
402: ERFEL WRKQSFHG KLHNF
1 A56236 ck: 8890 len: 1,220 ! probable RNA helicase 1 - human
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
538: NDIPE WKGHAFGG NKASY
1 S54293 ck: 5936 len: 1,083 ! regulator protein p122-RhoGAP - rat
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
393: NSSVN WRTGSFHG PGHLS
1 H71119 ck: 9251 len: 278 ! hypothetical protein PH0727 - Pyrococcus hc
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
99: PERVG WRVSSYMG ISFQN
1 G59435 ck: 9802 len: 1,091 ! DLC-1 (deleted in liver cancer), p122 [impo
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
401: NGSVN WRTGSFHG PGHIS
Databases searched:
NBRF, Release 76.1, Released on 12May2003, Formatted on 10Jun2003
Total finds: 98
Total length: 96,168,682
Total sequences: 283,308
CPU time: 02:12.67
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1 FINDPATTERNS on-swp:* allowing 0 mismatches
1 1 W(K,R)XX(S,A) (Y,F)XG January 12, 2004 10:19 ..
ADH3_ECOLI ck: 7661 len: 369 1 P25437 escherichia coli. alcohol dehydrogen
1 W(K,R)XX(S,A) (Y,F)XG
309: VTGRV WKGSAFPGG VKGRS
ADH3_HAEIN ck: 2043 len: 378 1 P44557 haemophilus influenzae. putative alcoh
1 W(K,R)XX(S,A) (Y,F)XG
318: VTGRV WKGSAFPGG VKGRS
ADH3_PASPI ck: 798 len: 369 1 P39450 pasteurella piscicida (photobacteriu
1 W(K,R)XX(S,A) (Y,F)XG
309: VTGRV WKGTAFFGG VKGRT
ADH1_GADMO ck: 1925 len: 375 1 P81600 gadus morhua (atlantic cod). alcohol
1 W(K,R)XX(S,A) (Y,F)XG
315: VTGRV WKGTAFFGG WKSVE
ADH1_RHOSH ck: 2905 len: 376 1 P72324 rhodobacter sphaeroides (rhodospseud
1 W(K,R)XX(S,A) (Y,F)XG
316: VTGRV WKGSAFPGG ARGRT
ADH1_GADMO ck: 1722 len: 375 1 P81601 gadus morhua (atlantic cod). alcohol
1 W(K,R)XX(S,A) (Y,F)XG
315: VTGRV WKGTAFFGG YKSVE
ADH1_ARATH ck: 5269 len: 379 1 Q96533 arabidopsis thaliana (mouse-ear cree
1 W(K,R)XX(S,A) (Y,F)XG
317: VTGRV WKGTAFFGG PKSRT
ADH1_CABEL ck: 9402 len: 384 1 Q17335 caenorhabditis elegans. alcohol dehy
1 W(K,R)XX(S,A) (Y,F)XG
321: VTGRV WKGTAFFGG WKSVE
ADH1_PROME ck: 8245 len: 378 1 P46415 drosophila melanogaster (fruit fly).
1 W(K,R)XX(S,A) (Y,F)XG
318: VTGRV WKGSAFPGG WRSVS
ADH1_HORSE ck: 6584 len: 373 1 P19854 equus caballus (horse). alcohol dehy
1 W(K,R)XX(S,A) (Y,F)XG
313: VTGRV WKGTAFFGG WKSVE
ADH1_UROHA ck: 5507 len: 373 1 P80467 uromastix hardwickii (indian spiny-t:
ADH1_HUMAN ck: 6689 len: 373 1 P11766 homo sapiens (human). alcohol dehydr
1 W(K,R)XX(S,A) (Y,F)XG
313: VTGRV WKGTAFFGG WKSVE
ADH1_MAIZE ck: 4477 len: 381 1 P93629 zea mays (maize). alcohol dehydrogen
1 W(K,R)XX(S,A) (Y,F)XG
319: VTGRV WKGTAFFGG FKGRS
ADH1_MOUSE ck: 8619 len: 373 1 P28474 mus musculus (mouse). alcohol dehydr
1 W(K,R)XX(S,A) (Y,F)XG
313: VTGRV WKGTAFFGG WKSVE
ADH1_MYXGL ck: 4299 len: 376 1 P80360 myxine glutinosa (atlantic hagfish).
1 W(K,R)XX(S,A) (Y,F)XG
316: VTGRV WKGRAFFGG WKSVE
ADH1_OCTVU ck: 6276 len: 378 1 P81431 octopus vulgaris (octopus). alcohol
1 W(K,R)XX(S,A) (Y,F)XG
316: VTGRV WKGTAFFGG FKSRD
ADH1_ORYSA ck: 4843 len: 381 1 P93436 oryza sativa (rice). alcohol dehydro
1 W(K,R)XX(S,A) (Y,F)XG
319: VTGRV WKGTAFFGG FKSRs
ADH1_PEA ck: 405 len: 378 1 P80572 pisum sativum (garden pea). alcohol
1 W(K,R)XX(S,A) (Y,F)XG
316: VTGRV WKGTAFFGG FKSRs
ADH1_RABIT ck: 5825 len: 373 1 O19053 oryctolagus cuniculus (rabbit). alco
1 W(K,R)XX(S,A) (Y,F)XG
313: VTGRV WKGTAFFGG WKSVE
ADH1_RAT ck: 6609 len: 373 1 P12711 rattus norvegicus (rat). alcohol dehy
1 W(K,R)XX(S,A) (Y,F)XG
313: VTGRV WKGTAFFGG WKSVE
ADH1_SPAAU ck: 6805 len: 376 1 P79896 sparus aurata (gilthead sea bream).
1 W(K,R)XX(S,A) (Y,F)XG
316: VTGRV WKGTAFFGG WKSVE
ADH1_UROHA ck: 5507 len: 373 1 P80467 uromastix hardwickii (indian spiny-t:
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309: VTGRV WRGSAFQG VKGRS  
 Q8XOU5 ck: 9212 len: 380 ! Q8x0u5 neurospora crassa. probable alcohol  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(A)(F)XG  
 319: VTGRV WRGSAFQG VKGRS  
 O74636 ck: 8858 len: 777 ! O74636 fusarium oxysporum. transposase-like  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(S)(F)XG  
 402: ERFEEI WRKQSPFG KLHNF  
 Q96V39 ck: 6889 len: 380 ! Q96v39 pichia angusta (yeast) (hansenula po  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(A)(F)XG  
 318: VTGRV WRGCAFGG IKGRT  
 Q8J2V2 ck: 8797 len: 230 ! Q8j2v2 gibberella zeae (fusarium graminearu  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(S)(F)XG  
 170: IDTDD WRYSFPG ABPSL  
 Q8JOF4 ck: 9502 len: 1,173 ! Q8jof4 penicillium citrinum. hmg-coa reduct  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(S)(F)XG  
 97: GPONG WKQSFPG DADVL  
 Q8JOF1 ck: 4488 len: 380 ! Q8jof1 candida boidinii (yeast). formaldehy  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(A)(F)XG  
 318: VTGRV WRGCAFGG VKGRT  
 Q8WZB3 ck: 404 len: 26,926 ! Q8wzb3 homo sapiens (human). n2b-titin iso  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(A)(Y)XG  
 18,126: NVTLK WKKPAYDG GSKIT  
 Q8NFW8 ck: 3639 len: 434 ! Q8nfw8 homo sapiens (human). cytidine monop  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(A)(Y)XG  
 365: EMGLC WKEVAYLG NEVSD  
 Q8WZ42 ck: 1298 len: 34,350 ! Q8wz42 homo sapiens (human). titin. 3/2003  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(A)(Y)XG  
 25,550: NVTLK WKKPAYDG GSKIT  
 Q8NB11 ck: 587 len: 496 ! Q8nb11 homo sapiens (human). hypothetical p  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(A)(Y)XG  
 4: MAL WRGSAYAG FLALA

Q8TC92 ck: 6092 len: 643 ! Q8tc92 homo sapiens (human). hypothetical f  
 W(K,R)XX(S,A)(Y,F)XG  
 W(K)XX(A)(F)XG  
 632: TLEKR WKLCAPEG IKTT  
 Q9NWE0 ck: 6755 len: 643 ! Q9nwe0 homo sapiens (human). hypothetical f  
 W(K,R)XX(S,A)(Y,F)XG  
 W(K)XX(A)(F)XG  
 632: TLEKR WKLCAPEG IKTT  
 Q9NQ20 ck: 2647 len: 434 ! Q9nqz0 homo sapiens (human). cmp-n-acetyln  
 W(K,R)XX(S,A)(Y,F)XG  
 W(K)XX(A)(Y)XG  
 365: EMGLC WKEVAYLG NEVSD  
 Q9BRR6 ck: 3596 len: 497 ! Q9brr6 homo sapiens (human). similar to rlb  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(A)(Y)XG  
 4: MAL WRGSAYAG FLALA  
 Q10466 ck: 227 len: 26,926 ! Q10466 homo sapiens (human). titin, heart  
 W(K,R)XX(S,A)(Y,F)XG  
 W(K)XX(A)(Y)XG  
 18,126: NVTLK WKKPAYDG GSKIT  
 Q96DQ2 ck: 9961 len: 811 ! Q96dq2 homo sapiens (human). hypothetical f  
 W(K,R)XX(S,A)(Y,F)XG  
 W(K)XX(S)(Y)XG  
 384: QINEN WKRHSYAG EQPET  
 Q8N0N4 ck: 7283 len: 99 ! Q8n0n4 branchiostoma floridae (florida lan  
 W(K,R)XX(S,A)(Y,F)XG  
 W(K)XX(A)(F)XG  
 39: VTGRV WKGTAFGG WKSVE  
 Q9NJD0 ck: 9928 len: 377 ! Q9njd0 branchiostoma floridae (florida lan  
 W(K,R)XX(S,A)(Y,F)XG  
 W(K)XX(A)(F)XG  
 317: VTGRV WKGTAFGG WKSVE  
 Q8WS90 ck: 6247 len: 377 ! Q8ws90 ciona intestinalis. alcohol dehydro  
 W(K,R)XX(S,A)(Y,F)XG  
 W(K)XX(A)(F)XG  
 317: VTGRT WKGTAFGG YKSVE  
 Q9NE65 ck: 4708 len: 1,778 ! Q9ne65 leishmania major. hypothetical 183.1  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)XX(S)(F)XG  
 1,309: VRVAS WRWSSFPF QJHSL  
 Q9NJC3 ck: 745 len: 377 ! Q9njc3 branchiostoma lanceolatum (common l  
 W(K,R)XX(S,A)(Y,F)XG

317: VTGRV	W(K,R)XX(A)(F)XG WKGTAFGG	WKSVD	Q9N356	ck: 7111	len: 317	1	Q9n356 caenorhabditis elegans. hypothetical
Q9BJ33	ck: 1200	len: 377	1	Q9bj33 branchiostoma floridae (florida land	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGTAFGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKQKSYDG VLAPF	241: VVQMT
317: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGTAFGG	WKSVE	Q9VA05	ck: 5184	len: 1,431	1	Q9va05 drosophila melanogaster (fruit fly).
Q9NP2	ck: 1806	len: 432	1	Q9nfp2 plasmodium falciparum. nima-related	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKAISYRG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKNVSPAG GIDNS	318: VVIAT
43: QEPFC	WKAISYRG	LKERE	Q8ISD5	ck: 9049	len: 1,057	1	Q8isd5 plasmodium falciparum (isolate 3d7).
Q965R0	ck: 8060	len: 554	1	Q965r0 caenorhabditis elegans. hypothetical	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGTAFGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKAISYRG LKERE	43: QEPFC
494: VTGRT	WKGTAFGG	WKSVE	Q95K71	ck: 1821	len: 414	1	Q95k71 macaca fascicularis (crab eating mac
Q9BJ34	ck: 835	len: 377	1	Q9bj34 branchiostoma floridae (florida land	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGTAFGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKLCAFGG IKTT	403: TLEKR
317: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGTAFGG	WKSVE	Q8WS89	ck: 6358	len: 377	1	Q8ws89 ciona intestinalis. alcohol dehydrog
Q9WS89	ck: 6358	len: 377	1	Q9ws89 ciona intestinalis. alcohol dehydrog	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGTAFGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(Y)XG W(K)XX(A)(Y)XG WKKPAYDG GSKIT	6,555: NVTLK
317: VTGRT	WKGTAFGG	YKSVE	Q9B394	ck: 8082	len: 255	1	Q9b394 blackburnia palmarum. cytochrome b (fr
Q18005	ck: 8316	len: 545	1	Q18005 caenorhabditis elegans. hypothetical	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG WRNSPFGG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG WRQMSFWG ATVIT	85: GYVLP
404: GLVGG	WRNSPFGG	FSNGV	Q9GI47	ck: 9519	len: 348	1	Q9gi47 daphniaphyllum sp. qiu 94162. mataras
Q97363	ck: 7232	len: 313	1	Q97363 bombyx mori (silk moth). lipopolysac	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKDVAFIG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG W(K)XX(S)(F)XG WKNNSFLG HNKNL	77: ISAND
230: MIGSF	WKDVAFIG	FHDWN	Q38144	ck: 957	len: 159	1	Q38144 bacteriophage appl. required for rep
Q961U1	ck: 4884	len: 1,721	1	Q961u1 drosophila melanogaster (fruit fly).	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRPPSYDG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG WRTGAPEG QDGKR	77: GVSQS
253: SCHLN	WRPPSYDG	GLKVS	Q9B0E2	ck: 7287	len: 412	1	Q9b0e2 staphylococcus aureus temperate phag
Q9NBV9	ck: 7429	len: 327	1	Q9nbv9 manduca sexta (tobacco hawkmoth) (to	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKDNAPVG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKNRSEFWG VINNT	35: YDFSP
232: MVGNF	WKDNAPVG	FHDWG	Q8S9Y0	ck: 4807	len: 929	1	Q8s9y0 oryza sativa (japonica cultivar-group
Q9V4F7	ck: 9013	len: 8,971	1	Q9v4f7 drosophila melanogaster (fruit fly).	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRPPSYDG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG WRVHAYKG KWNDY	266: KBDCP
7,429: SCHLN	WRPPSYDG	GLKVS	Q8RUM3	ck: 5321	len: 542	1	Q8rum3 oryza sativa (japonica cultivar-group



1 W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(Y)XG KLFMV  
247: FGRPC WRTLSYQG

1 Q9FW81 ck: 4017 len: 1,626 | Q9fw81 oryza sativa (rice). mutator-like tr  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q8LR53 ck: 1421 len: 1,605 | Q8lr53 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q8LQ12 ck: 4995 len: 1,592 | Q8lq12 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q9FRA2 ck: 2655 len: 1,011 | Q9fra2 oryza sativa (rice). similar to oryza  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 277: KDGCP WRVHAYKG

1 Q947Y7 ck: 3231 len: 2,421 | Q947y7 oryza sativa (rice). putative mutat  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 172: KEDCP WRVHAYKG

1 Q94D87 ck: 3033 len: 1,626 | Q94d87 oryza sativa (rice). putative mutat  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q9AYG3 ck: 3386 len: 1,641 | Q9ayg3 oryza sativa (rice). mutator-like tr  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q9LDW9 ck: 2865 len: 1,591 | Q9ldw9 oryza sativa (rice). est c28952(c629  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q8W5M7 ck: 4750 len: 1,597 | Q8w5m7 oryza sativa (rice). putative mutat  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q94FB8 ck: 695 len: 2,910 | Q94fb8 schizochytrium sp. atcc\_20888. poly  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(F)XG FLGNV

1 181: ANFPE WRLDSFEG

1 Q9LDE7 ck: 51 len: 938 | Q9lde7 oryza sativa (rice). est c28952(c629  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q8W3H2 ck: 8786 len: 1,638 | Q8w3h2 oryza sativa (rice). mutator-like tr  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q9FGN6 ck: 275 len: 895 | Q9fgn6 arabidopsis thaliana (mouse-ear cres  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(F)XG LPHFT

1 621: RSQCQ WQWSPAG

1 Q94LE7 ck: 4734 len: 883 | Q94le7 oryza sativa (rice). putative transf  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG VEKYH

1 266: KEDCP WRVHAYKG

1 Q8SB37 ck: 39 len: 1,656 | Q8sb37 oryza sativa (rice). putative transf  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEECP WRVHAYKG

1 Q9T0J6 ck: 7947 len: 700 | Q9t0j6 arabidopsis thaliana (mouse-ear cres  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(Y)XG RDDL E

1 645: PQQIN WRPPSYFG

1 Q8S5Y6 ck: 7546 len: 1,557 | Q8s5y6 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 266: KEDCP WRVHAYKG

1 Q8S696 ck: 8699 len: 1,530 | Q8s696 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG KWN DY

1 271: KDGCP WRVHAYKG

1 Q8S1F8 ck: 8647 len: 1,080 | Q8s1f8 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(F)XG AGDEQ

1 742: AVFDN WRMPAPAG

1 O04892 ck: 2338 len: 530 | O04892 nicotiana tabacum (common tobacco).  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(F)XG GNDY

1 254: RGCSP WRDPAPVG

1 O64761 ck: 1756 len: 303 | O64761 arabidopsis thaliana (mouse-ear cres

1 15: IPGPK W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG MQIGY  
Q9LDA3 ck: 5721 len: 1,281 ! Q91da3 oryza sativa (rice). est c28952(c629)

1 237: KEDCP WRVHAYKG KWNDY  
Q8LSZ5 ck: 7458 len: 602 ! Q81ez5 physcomitrella patens (moss). ferred

1 394: LIDPS WKRSFPFG VNPQK  
Q8W062 ck: 1142 len: 1,604 ! Q8w062 oryza sativa (rice), and oryza sativ

1 266: KEDCP WRVHAYKG KWNDY  
O82014 ck: 9934 len: 396 ! O82014 linum usitatissimum (flax) (linseed)

1 340: FLVGR WKVDAFTG LSSEG  
Q8S521 ck: 6884 len: 198 ! Q8s521 zea mays (maize). d-type cyclin (fza

1 97: AIDWI WKVHAYYG FGPLT  
Q8S211 ck: 4528 len: 1,353 ! Q8s211 oryza sativa (japonica cultivar-grou

1 265: KEDCP WRVHAYKG KWNDY  
Q94E86 ck: 1244 len: 603 ! Q94e86 oryza sativa (rice). b1045d11.16 prc

1 410: QTNLS WKYMAFQG KIYAA  
Q9XE23 ck: 820 len: 955 ! Q9xe23 oryza sativa (rice). est c28952(c629

1 115: KEDCP WRVHAYKG KWNDY  
Q8LN97 ck: 3122 len: 1,536 ! Q8ln97 oryza sativa (japonica cultivar-grou

1 266: KEDCP WRVHAYKG KWNDY  
Q8LN69 ck: 2184 len: 655 ! Q8ln69 oryza sativa (japonica cultivar-grou

266: KEDCP WRVHAYKG KWNDY  
Q8RYT2 ck: 5760 len: 1,110 ! Q8ryt2 oryza sativa (japonica cultivar-grou

209: KEDCP WRVHAYKG KWNDY  
Q9SBA2 ck: 9787 len: 396 ! Q9sba2 linum usitatissimum (flax) (linseed)

340: FLVGR WKVDAFTG LSSEG  
Q94JG7 ck: 2586 len: 429 ! Q94jg7 oryza sativa (rice), and oryza sativ

347: RDMV WKVKSFPFG GKDYM  
O22715 ck: 2687 len: 428 ! O22715 arabidopsis thaliana (mouse-ear cres

346: KDALV WKIKSFPFG NKEYM  
Q9SW79 ck: 8565 len: 274 ! Q9sw79 triticum aestivum (wheat). alternati

21: GRRRR WRISYWG IEQSK  
Q8H904 ck: 6567 len: 1,597 ! Q8h904 oryza sativa (japonica cultivar-grou

266: KEDCP WRVHAYKG KWNDY  
Q8H8E2 ck: 1340 len: 779 ! Q8h8e2 oryza sativa (japonica cultivar-grou

266: KEDCP WRVHAYKG KWNDY  
Q8H7V5 ck: 7087 len: 1,596 ! Q8h7v5 oryza sativa (japonica cultivar-grou

277: KDGP WRVHAYKG KWKDY  
Q8H5S9 ck: 5613 len: 1,179 ! Q8h5s9 oryza sativa (japonica cultivar-grou

273: KDGP WRVHAYKG KWKDY  
Q8H525 ck: 8356 len: 1,727 ! Q8h525 oryza sativa (japonica cultivar-grou

266: KEDCP WRVHAYKG KWNDY  
Q8H525 ck: 8356 len: 1,727 ! Q8h525 oryza sativa (japonica cultivar-grou

1 Q8H4Y6 ck: 2309 len: 268 ! Q8h4y6 oryza sativa (japonica cultivar-group)  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(F)XG  
243: PFRSP WRAVSFG ARRSV

1 Q8H2L9 ck: 9400 len: 1,662 ! Q8h2l9 oryza sativa (japonica cultivar-group)  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG  
266: KEDCP WRVHAYKG KWNDY

1 Q8H2L7 ck: 8873 len: 1,753 ! Q8h2l7 oryza sativa (japonica cultivar-group)  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG  
266: KEDCP WRVHAYKG KWNDY

1 Q8GX38 ck: 3045 len: 265 ! Q8gx38 arabidopsis thaliana (mouse-ear cre  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(Y)XG  
210: PQQIN WRPPSYFG RDDLE

1 Q8GRQ7 ck: 3759 len: 903 ! Q8grq7 oryza sativa (japonica cultivar-group)  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG  
266: KSECP WRVHAYKG KWNDY

1 Q88719 ck: 9067 len: 432 ! Q88719 mus musculus (mouse). cmp-n-acetylne  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
363: EMGLC WKEVAYLG NEVSD

1 Q8RSB1 ck: 3258 len: 490 ! Q8rsb1 mus musculus (mouse). similar to hyp  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8K2G7 ck: 8878 len: 432 ! Q8k2g7 mus musculus (mouse). cytidine monoph  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
363: EMGLC WKEVAYLG NEVSD

1 Q99KK2 ck: 2584 len: 166 ! Q99kk2 mus musculus (mouse). similar to cyto  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
97: EMGLC WKEVAYLG NEVSD

1 Q9JHG0 ck: 2510 len: 197 ! Q9jhg0 mus musculus (mouse). cbln3. 6/2001  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(S)(F)XG  
184: NLILGG WKYSFSG FLIFP

1 Q8C662 ck: 221 len: 374 ! Q8c662 mus musculus (mouse). alcohol dehydro  
W(K,R)XX(S,A)(Y,F)XG

314: VTGRT W(K)XX(A)(F)XG  
WKGTAFGG WKSVE

1 Q8C330 ck: 6000 len: 200 ! Q8c330 mus musculus (mouse). cytidine monoph  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
131: EMGLC WKEVAYLG NEVSD

1 Q8BY11 ck: 241 len: 305 ! Q8by11 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BXA6 ck: 890 len: 224 ! Q8bxa6 mus musculus (mouse). similar to ch  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(F)XG  
30: TLLPQ WRVSAFIG SNIII

1 Q8BWI1 ck: 675 len: 689 ! Q8bwy1 mus musculus (mouse). hypothetical  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(S)(Y)XG  
384: QLNNEN WKRHSYAG EQPET

1 Q8BJ63 ck: 3056 len: 490 ! Q8bj63 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BJ58 ck: 6723 len: 398 ! Q8bj58 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BJ31 ck: 3487 len: 307 ! Q8bj31 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BI12 ck: 3107 len: 490 ! Q8bi12 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BHR2 ck: 4917 len: 643 ! Q8bhr2 mus musculus (mouse). hypothetical  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(F)XG  
632: TLEKR WKLCAFEG IKTT

1 Q91TT0 ck: 2878 len: 138 ! Q91tt0 tupaia herpesvirus. t22.9. 10/2002  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(F)XG  
67: TSVPV WRLCSFGG GFVLG

1	Q8V715	ck: 8144	len: 547	! Q8v715 swine calicivirus. capsid protein. 6	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	73: DVKQK WRCVAYPG	NGFVS	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	
	410: QDPNQ	WRLPAYGG	ALTNN							
1	Q8QNH4	ck: 1050	len: 284	! Q8qnh4 ectocarpus siliculosus virus. esv-1	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	Q90XR4	ck: 7881	len: 210	! Q90xr4 brachydanio rerio (zebrafish) (danio)
	75: NCLKN	WKPEAFLG	SGAHG				27: CALPM	WKVTAFIG	TNIVV	
1	Q9QQN6	ck: 7259	len: 479	! Q9qqn6 sugarcane yellow leaf virus. putative	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	Q90XR8	ck: 4395	len: 215	! Q90xr8 brachydanio rerio (zebrafish) (danio)
	129: ANLAG	WRAYAYSG	CTISN				30: CALPM	WKVTAFIG	ANIVT	
1	Q66159	ck: 2936	len: 159	! Q66159 cauliflower mosaic virus. orf ii. 6/	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XR0	ck: 4854	len: 214	! Q90xr0 brachydanio rerio (zebrafish) (danio)
	61: SLLGI	WKINSYFG	LSKDP				29: CALPM	WRVSAFVG	ANIVT	
1	Q83166	ck: 3141	len: 159	! Q83166 cauliflower mosaic virus. aphid trans	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XR9	ck: 2537	len: 209	! Q90xr9 brachydanio rerio (zebrafish) (danio)
	61: SLLGI	WKINSYFG	LSKDP				30: CALPM	WKVTAFIG	ANIVT	
1	Q83179	ck: 3686	len: 159	! Q83179 cauliflower mosaic virus. orf ii protein	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q9DE12	ck: 435	len: 214	! Q9de12 xenopus laevis (african clawed frog)
	61: SLLGI	WKINSYFG	LSKDP				30: CALPM	WRVTAFIG	NNIVV	
1	Q9JH75	ck: 3583	len: 479	! Q9jh75 sugarcane yellow leaf virus. putative	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	Q90XR6	ck: 1235	len: 211	! Q90xr6 brachydanio rerio (zebrafish) (danio)
	129: ANLAG	WRAYAYSG	CTISN				30: IAIPQ	WKTSAFIG	QNIIT	
1	Q9WI33	ck: 2997	len: 159	! Q9wi33 cauliflower mosaic virus. aphid trans	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XR2	ck: 5577	len: 218	! Q90xr2 brachydanio rerio (zebrafish) (danio)
	61: SLLGI	WKINSYFG	LSKDP				30: CALPM	WRVTAFIG	TNIVT	
1	Q83157	ck: 8743	len: 64	! Q83157 cauliflower mosaic virus. aphid acquisition	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XD4	ck: 5678	len: 376	! Q90xd4 brachydanio rerio (zebrafish) (danio)
	7: SLLGI	WKINSYFG	LSKDP				316: VTGRT	WKGTAFIG	WKSVE	
1	Q83162	ck: 8680	len: 99	! Q83162 cauliflower mosaic virus. hypothetical	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XQ9	ck: 100	len: 214	! Q90xq9 xenopus laevis (african clawed frog)
	61: SLLGI	WKINSYFG	LSKDP				30: CAMP	WRVTAFIG	NNIVV	
1	Q8V2M7	ck: 663	len: 146	! Q8v2m7 camelpox virus (strain cp-1). hypothetical	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	Q98SR2	ck: 3404	len: 214	! Q98sr2 gallus gallus (chicken). claudin-3. 1
							29: CALPM	WRVTAFIG	NNIVT	

1	Q90XQ8	ck: 8089	len: 210	! Q90xq8 brachydanio rerio (zebrafish) (danio)	1	VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	318: VKGRS
1	30: TAMAE	WNMSSYAG	DNIIT						
1	Q8UVX9	ck: 8315	len: 209	! Q8uvx9 torpedo marmorata (marbled electric)	1		W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(Y)XG	Q911E5 ck: 8784 len: 538 ! Q911e5 pseudomonas aeruginosa. probable sul
1	90: QSSCA	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K)XX(S)(F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	1	VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	455: VRSER WKYIAYDG FRAQL
1	Q90WG6	ck: 4720	len: 432	! Q90wg6 oncorhynchus mykiss (rainbow trout)	1		W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	Q9HY01 ck: 6470 len: 370 ! Q9hy01 pseudomonas aeruginosa. alcohol dehy
1	355: DKDLD	WKEVAYMG	NDAPD				W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	310: VTGRV WKGSAFGG VGRS
1	Q8JIE6	ck: 8389	len: 1,019	! Q8jie6 gallus gallus (chicken). hira. 3/200	1		W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	Q9HT72 ck: 5958 len: 262 ! Q9ht72 pseudomonas aeruginosa. permease of
1	97: KLIMV	WKEAAYIG	PSTVP				W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	28: GSFVV WRRMAYFG DTLSH
1	Q8AVG4	ck: 4992	len: 211	! Q8avg4 xenopus laevis (african clawed frog)	1		W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	Q9CP25 ck: 9951 len: 261 ! Q9cp25 pasteurella multocida. hypothetical
1	30: IAIPO	WKMSSFAG	DAIIT				W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	28: GAFVV WKKMAYFG DTLAH
1	Q8Q7G3	ck: 8999	len: 861	! Q8q7g3 human immunodeficiency virus 1. env	1		W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	Q9A956 ck: 9243 len: 613 ! Q9a956 caulobacter crescentus. tonb-depende
1	777: LASGI	W(RVNSYL	LGLGI				W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	370: KGDTW WRAAYAG FRPPT
1	O67832	ck: 5280	len: 392	! O67832 aquifex aeolicus. hypothetical prote	1		W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	Q9A5D4 ck: 8539 len: 369 ! Q9a5d4 caulobacter crescentus. alcohol dehy
1	127: YVSVN	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K)XX(S)(F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	1	VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	309: ARGRT WKGTAFGG
1	Q9KQB7	ck: 3098	len: 260	! Q9kqb7 vibrio cholerae. zinc abc transporte	1		W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	Q988W5 ck: 8644 len: 700 ! Q988w5 rhizobium loti (mesorhizobium loti).
1	28: GSFVV	W(RMAYFG	DTLAH				W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG	379: ELLGP WRKFAFHG AGACT
1	Q9KPP6	ck: 9551	len: 1,208	! Q9kpp6 vibrio cholerae. exodeoxyribonuclea	1		W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG	Q987D8 ck: 5716 len: 412 ! Q987d8 rhizobium loti (mesorhizobium loti).
1	906: AIDRR	W(RVTSYSG	LVMQS				W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG	315: NIEAA WRWVSFWG QTDAA
1	Q9KCG9	ck: 2788	len: 540	! Q9kcg9 bacillus halodurans. d-3-phosphoglyc	1		W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	Q984R5 ck: 9706 len: 219 ! Q984r5 rhizobium loti (mesorhizobium loti).
1	141: IKAGE	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	W(K)XX(S)(Y)XG W(K)XX(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	1	CMDAA	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	148: KQORI WRSKSYKG
1	Q9JRB0	ck: 788	len: 378	! Q9jrb0 neisseria meningitidis (serogroup a)	1		W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	Q983F3 ck: 2074 len: 344 ! Q983f3 rhizobium loti (mesorhizobium loti).

264: RDIKI WRSVSYIG LISYP  
 Q8ZPA8 ck: 2185 len: 372 | Q8zpa8 salmonella typhimurium. alcohol dehy  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(F)XG  
 309: VTGRV WRGSAPFG VKGRT  
 Q8ZNV6 ck: 6897 len: 261 | Q8zmv6 salmonella typhimurium. abc superfam  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 28: GSFVV WRRMSYFG DTLAH  
 Q8ZN10 ck: 8280 len: 199 | Q8zn10 salmonella typhimurium. gifsy-1 prop  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(F)XG  
 180: WRHRA WRASAPFG ICNDF  
 Q8ZMB6 ck: 4862 len: 1,181 | Q8zmb6 salmonella typhimurium. exonuclease  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 901: LLYDS WRVTSYSG LQORG  
 Q8ZH88 ck: 4557 len: 1,220 | Q8zh88 yersinia pestis. exodeoxyribonucleas  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 904: KMQDY WRVTSYSG LQSG  
 Q8ZG44 ck: 7342 len: 766 | Q8zg44 yersinia pestis. hypothetical protei  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 306: ADAPL WRTISYFG GKGVV  
 Q8ZG18 ck: 6334 len: 377 | Q8zg18 yersinia pestis. probable alcohol de  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(F)XG  
 310: VTGRV WRGSAPFG VKGRS  
 Q8Z6M8 ck: 4455 len: 122 | Q8z6m8 salmonella typhi. putative pathogeni  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(F)XG  
 70: KALAN WKPAAFQG IPQRL  
 Q8Z5W5 ck: 7341 len: 261 | Q8z5w5 salmonella typhi. high-affinity zinc  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 28: GSFVV WRRMSYFG DTLAH  
 Q8Z419 ck: 4255 len: 1,181 | Q8z419 salmonella typhi. exonuclease v sub  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 901: LLYDS WRVTSYSG LQORG

Q8YTB3 ck: 892 len: 369 | Q8ytb3 anabaena sp. (strain pcc 7120). glut  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(F)XG  
 309: VTGRV WRGSAPFG ARGRT  
 Q8XCJ0 ck: 7492 len: 261 | Q8xcj0 escherichia coli o157:h7. orf, hypot  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 28: GSFVV WRRMSYFG DTLAH  
 Q8X847 ck: 2142 len: 247 | Q8x847 escherichia coli o157:h7. putative t  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(F)XG  
 228: WRHRA WRASAPFG ICNDL  
 Q8X7X8 ck: 6047 len: 215 | Q8x7x8 escherichia coli o157:h7. hypothetical  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(F)XG  
 65: VTDPQ WRNKAFFG LKDPE  
 Q8X6M9 ck: 2018 len: 1,180 | Q8x6m9 escherichia coli o157:h7. dna helica  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 901: LPQDN WRVTSYSG LQORG  
 Q8X5J4 ck: 7697 len: 369 | Q8x5j4 escherichia coli o157:h7. alcohol de  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(F)XG  
 309: VTGRV WRGSAPFG VKGRS  
 Q8UF80 ck: 5850 len: 298 | Q8uf80 agrobacterium tumefaciens (strain c5  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(Y)XG  
 55: GCFVV WRRMAYFG DTMAH  
 Q8X3C3 ck: 8152 len: 227 | Q8x3c3 escherichia coli o157:h7. hypothetical.  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(Y)XG  
 35: DEIKY WRYTSYNG GKLUPE  
 Q9ACP5 ck: 2721 len: 1,039 | Q9acp5 streptomyces coelicolor. putative la  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(A)(Y)XG  
 603: GGAFA WKVRAYDG SAYSA  
 Q9RRD0 ck: 3668 len: 206 | Q9rrd0 deinococcus radiodurans. 3-demethylu  
 W(K,R)XX(S,A)(Y,F)XG  
 W(R)xx(S)(F)XG  
 111: VBETG WRTASPDG VVUGA  
 Q92P77 ck: 5059 len: 275 | Q92p77 rhizobium meliloti (sinorhizobium me.  
 W(K,R)XX(S,A)(Y,F)XG

29: GCFVI	W(R)xx(A)(Y)XG WRRMAYFG	DTMAH		Q8PPF2	ck: 6865	len: 369	! Q8ppf2 xanthomonas axonopodis (pv. citri).
Q8VEQ9	ck: 9722	len: 370	! Q8yeq9 brucella melitensis. alcohol dehydrogenase	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	VKGRV	
310: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGTAFFG	ARGRT				
Q8YDJ9	ck: 8470	len: 284	! Q8yjd9 brucella melitensis. high-affinity iron uptake	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	WRRMAYFG	
40: GCFII	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	WRRMAYFG	DTMAH				
Q8YIT4	ck: 3386	len: 368	! Q8yit4 ralstonia solanacearum (pseudomonas)	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGSAFFG	
308: VTGRE	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGSAFFG	ARGRT				
Q8XTN7	ck: 4468	len: 368	! Q8xtn7 ralstonia solanacearum (pseudomonas)	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGSAFFG	
308: VTGRE	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	WKGSAFFG	VLPT				
Q8RHM9	ck: 4108	len: 454	! Q8rhm9 fusobacterium nucleatum (subsp. nucleatum)	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	WKGSAFFG	
226: EIKSN	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	WKGSAFFG	VLPT				
Q8REQ9	ck: 5980	len: 303	! Q8req9 fusobacterium nucleatum (subsp. nucleatum)	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	WKGSAFFG	
216: NIFLS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	WKGSAFFG	FLSSG				
Q8R8C0	ck: 4513	len: 474	! Q8r8c0 thermoanaerobacter tengcongensis. 8	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	WKGSAFFG	
446: KQGGK	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	WKGSAFFG	VYNPV				
Q8R6S5	ck: 1574	len: 835	! Q8r6s5 thermoanaerobacter tengcongensis. hy	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGSAFFG	
608: YGSPT	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGSAFFG	TLNGA				
Q8PPQ7	ck: 6719	len: 697	! Q8ppq7 xanthomonas axonopodis (pv. citri).	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGSAFFG	
374: PSPDG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGSAFFG	APSPG				
Q8PPN3	ck: 2843	len: 368	! Q8ppn3 xanthomonas axonopodis (pv. citri).	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	WKGSAFFG	
308: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	WKGSAFFG	VKGRS				

1	35: YDFSP	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKKKSPWG	VINNT	Q9EWW0	ck: 2209	len: 266	! Q9eww0 streptomyces coelicolor. putative en
1	Q8NSQ2	ck: 387	len: 275	! Q8neq2 corynebacterium glutamicum (brevibac	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG W(K)xx(S)(F)XG	WRSVAPSG	DRAEG
1	130: AAVIG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG WKDLAYAG	VIDSG	Q8ZHD4	ck: 8384	len: 765	! Q8zhd4 yersinia pestis. putative kinase (hy
1	Q8NSJ2	ck: 6981	len: 301	! Q8nej2 corynebacterium glutamicum (brevibac	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	WRTISYFG	GKGVV
1	254: AKRNW	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKLISPTG	IGSVV	Q8ZEU4	ck: 7586	len: 261	! Q8zeu4 yersinia pestis. high-affinity zinc
1	Q8NQY7	ck: 9818	len: 530	! Q8ngy7 corynebacterium glutamicum (brevibac	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	WRRMSYFG	DTLAH
1	132: LREGE	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKRSSFNG	VEIFG	Q8G857	ck: 8641	len: 366	! Q8g857 bifidobacterium longum. permease pro
1	Q9S2V4	ck: 1160	len: 330	! Q9s2v4 streptomyces coelicolor. putative me	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	WRWPAFAG	LPSPS
1	31: KARLR	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRLIAPAG	FVGVV	Q8FUU4	ck: 2536	len: 286	! Q8fuu4 brucella suis. zinc abc transporter,
1	Q9RK55	ck: 2102	len: 519	! Q9rkb5 streptomyces coelicolor. monooxygena	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WRRMAYFG	DTMAH
1	50: SVGGT	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRDNSYFG	CACDV	Q8FRY1	ck: 419	len: 254	! Q8fry1 corynebacterium efficiens. hypotheti
1	Q9RD13	ck: 4085	len: 660	! Q9rd13 streptomyces coelicolor. putative re	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	WREFAYAG	VVESG
1	135: AALGE	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRGPAYAG	FGAAD	Q8FPV9	ck: 8770	len: 530	! Q8fpv9 corynebacterium efficiens. putative
1	Q9RDQ2	ck: 398	len: 65	! Q9rdq2 streptomyces coelicolor. hypothetical	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WKRSSFNG	VEIFG
1	12: LSNVE	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRKSSYSG	SNGGD	Q8FKP5	ck: 7207	len: 715	! Q8fkp5 escherichia coli o6. putative cytopl
1	Q9RD18	ck: 4543	len: 65	! Q9rd18 streptomyces coelicolor. hypothetical	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WRFRAYYG	QVIVA
1	7: SIMDN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRRSSYSG	PGDGN	Q8PKG1	ck: 8529	len: 369	! Q8pkg1 escherichia coli o6. alcohol dehydro
1	Q9RD17	ck: 8793	len: 65	! Q9rd17 streptomyces coelicolor. hypothetical	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WKGSAFGG	VKGRS
1	7: RRMDN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRKSSYSG	PDDGN	Q8FI60	ck: 9281	len: 247	! Q8fi60 escherichia coli o6. putative tail co
1	Q9ADD0	ck: 1282	len: 243	! Q9add0 streptomyces coelicolor. hypothetical	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WKAASFLG	WRASAPTG	IYNDL
1	47: HRGHR	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WKAASFLG	VDEVY	Q8FGR4	ck: 7660	len: 261	! Q8fgr4 escherichia coli o6. high-affinity z



1	28: GSFVV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	DTLAH	314: VTGRV	WKSAPFG	VKGRS
1	Q8FG68	ck: 9474 len: 261	Q8fg68 escherichia coli o6. hypothetical ph	Q8DWE2	ck: 8469 len: 372	Q8dwe2 streptococcus mutans. putative alcohol
1	71: DEIKY	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	GEFPE	312: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFPG	VKGKT
1	904: LPGDN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	LQORG	Q8DJN0	ck: 1651 len: 399	Q8djn0 synschochoccus elongatus (thermosyns
1	Q8F6V8	ck: 4588 len: 1,183	Q8feb3 escherichia coli o6. exodeoxyribonuc	258: HNOVY	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRNOSYTG	FGMGA
1	136: VTDFI	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WRGLSPSG	EMANR	Q8DFQ3	ck: 1793 len: 265	Q8dfq3 vibrio vulnificus. abc-type mn2+/zn2
1	Q8F4M6	ck: 7773 len: 523	Q8f6v8 leptospira interrogans. putative out	32: GSFVV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRIMAYFG	DTLAH
1	244: QISSN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WKDPSPEG	SFLPK	Q8DF77	ck: 391 len: 376	Q8df77 vibrio vulnificus. zn-dependent alco
1	Q8F2V5	ck: 8001 len: 749	Q8f2v5 leptospira interrogans. inner membra	315: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFPG	VKGRS
1	284: LESPI	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WRLASPEG	VELKD	Q8DBL8	ck: 5828 len: 1,206	Q8dbl8 vibrio vulnificus. atp-dependent exo
1	Q8EYP7	ck: 6380 len: 403	Q8eyp7 leptospira interrogans. argininosucc	909: PIDRL	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRITSYSG	LVKQG
1	149: TIIAP	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WRIWSFGG	RSDLI	Q8D386	ck: 9466 len: 265	Q8d386 wiggleworthia bravipalpis. yebe pro
1	Q8EXC1	ck: 4765 len: 249	Q8exc1 leptospira interrogans. probable sug	28: GSFII	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRKMSYFG	DTLSH
1	211: KYMTS	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WKSFSYSG	EPRKL	Q8D070	ck: 2620 len: 379	Q8d070 yersinia pestis. alcohol dehydrogena
1	Q8BFC7	ck: 2100 len: 379	Q8bfc7 shewanella oneidensis. alcohol dehyd	312: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFPG	VKGRS
1	317: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFPG	VKGRS	Q8CZY3	ck: 1453 len: 1,241	Q8czy3 yersinia pestis. dna helicase, atp-d
1	Q8BF45	ck: 5478 len: 1,259	Q8bf45 shewanella oneidensis. exodeoxyribor	925: KMQDY	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVTSYSG	LQOSG
1	949: QYRTP	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVGSYSG	LVKNA	Q8CKW8	ck: 7447 len: 766	Q8ckw8 yersinia pestis. hypothetical. 3/200
1	Q8B800	ck: 4584 len: 376	Q8e800 shewanella oneidensis. zinc-binding	306: ADAPL	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTISYSG	GKGVV
1				O58458	ck: 9251 len: 278	O58458 pyrococcus horikoshii. hypothetical
1				99: PERVG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVSSYMG	ISFQN

Q97YM4 ck: 5165 len: 422 ! Q97ym4 sulfolobus solfataricus. n-acetylglu  
 1 W(K,R)XX(S,A)(Y,P)XG  
 W(R)xx(S)(Y)XG  
 415: YGVSE WRGSSYLQ

Q8THB2 ck: 6769 len: 355 ! Q8thb2 methanosarcina acetivorans. iron(iii)  
 1 W(K,R)XX(S,A)(Y,P)XG  
 W(R)xx(A)(P)XG FLLLP  
 24: PFCLE WRSAPIG

Q8Q0X8 ck: 4651 len: 535 ! Q8q0x8 methanosarcina mazei (methanosarcina  
 1 W(K,R)XX(S,A)(Y,P)XG  
 W(K)xx(A)(Y)XG NTGFG  
 469: QAIEN WKLAAYDG

Databases searched:  
 SWISS-PROT, Release 41.1, Released on 6Jun2003, Formatted on 9Jun2003  
 SPTREMBL, Release 23.0, Released on 4Mar2003, Formatted on 7Mar2003

Total finds: 336  
 Total length: 305,079,309  
 Total sequences: 958,388  
 CPU time: 07:35.08

!!AA SEQUENCE 1.0  
ID -AAB06419 standard; peptide; 8 AA.  
XX  
AC AAB06419;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PP 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1999; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 39; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 8 AA;

AAB06419 Length: 8 January 12, 2004 11:03 Type: P Check: 2784 ..

1 WKIYSVAG

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!!AA SEQUENCE 1.0
ID AAB06420 standard; peptide; 9 AA.
AC AAB06420;
DT 28-SEP-2000 (first entry)
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 476.
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX Mammalia.
XX OS
XX PN WO200026360-A1.
XX PD 11-MAY-2000.
XX PF 03-NOV-1999; 99WO-CA01029.
XX PR 03-NOV-1998; 98US-0185908.
XX PR 30-MAR-1999; 99US-0282029.
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuck OW, Symonds JM, Gour BJ;
XX DR WPI; 2000-365610/31.
XX PT Antibody modulation of claudin-mediated cell adhesion for increasing
XX PT vasopermeability, for delivering drugs to tumors and the nervous system
XX PT and across the skin -
XX PS Claim 39; Page 96; 121pp; English.
XX CC The present invention relates to the use of peptides as claudin-mediated
XX CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
XX CC which are membrane glycoproteins involved in cell adhesion. In some
XX CC situations, cell adhesion occurs at abnormal levels, and these peptides
XX CC can be used to modulate these levels, and thus treat autoimmune diseases,
XX CC inflammatory diseases and cancer, and aid wound healing and implant
XX CC adhesion. In addition, they can also be used to facilitate drug delivery
XX CC to the desired target site.
XX SQ Sequence 9 AA;

```

AAB06420 Length: 9 January 12, 2004 11:03 Type: P Check: 3486 ..

1 WKIYSYAGN

!!AA SEQUENCE 1.0  
ID -AAB06426 standard; peptide; 8 AA.  
XX  
AC AAB06426;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
XX and across the skin -  
XX  
PS Claim 39; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 8 AA;

AAB06426 Length: 8 January 12, 2004 11:03 Type: P Check: 2798 ..

1 WRIYSYAG

!!AA SEQUENCE 1.0  
ID AAB06427 standard; peptide; 9 AA.  
XX  
AC AAB06427;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 486.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
XX Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 39; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 9 AA;

AAB06427 Length: 9 January 12, 2004 11:03 Type: P Check: 3500 ..

1 WRIYSYAGN

```

!!AA SEQUENCE 1.0
ID AAB06436 standard; peptide; 10 AA.
AC AAB06436;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 67.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06436 Length: 10 January 12, 2004 11:03 Type: P Check: 4153 ..

1 CWKIYSYAGC

!!AA SEQUENCE 1.0  
ID AAB06445 standard; peptide; 10 AA.  
AC AAB06445;  
XX 28-SEP-2000 (first entry)  
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 76.  
DE Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX Mammalia.  
OS  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06445 Length: 10 January 12, 2004 11:03 Type: P Check: 4171 ..

1 KWKIYSYAGD



!!AA SEQUENCE 1.0  
ID AAB06454 standard; peptide; 10 AA.  
XX  
AC AAB06454;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 85.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06454 Length: 10 January 12, 2004 11:03 Type: P Check: 4181 ..

1 KWKIYSYAGE

```

!!AA SEQUENCE 1.0
ID AAB06463 standard; peptide; 10 AA.
AC AAB06463;
DT 28-SEP-2000 (first entry)
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 94.
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
OS Mammalia.
PN WO200026360-A1.
XX 11-MAY-2000.
XX 03-NOV-1999; 99WO-CA01029.
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX Claim 43; Page 97; 121pp; English.
XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-1 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site. The present sequence has a cyclic
XX conformation.
SQ Sequence 10 AA;

```

AAB06463 Length: 10 January 12, 2004 11:04 Type: P Check: 4234 ..

1 DWKIYSYACK

!!AA SEQUENCE 1.0  
ID AAB06472 standard; peptide; 10 AA.  
XX  
AC AAB06472;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 103.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1999; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 97; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06472 Length: 10 January 12, 2004 11:04 Type: P Check: 4235 ..  
1 EWKIYSYAGK

!!AA SEQUENCE 1.0  
ID AAB06479 standard; peptide; 8 AA.  
XX  
AC AAB06479;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 97; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 8 AA;  
AAB06479 Length: 8 January 12, 2004 11:04 Type: P Check: 2784 ..  
1 WKIYSYAG

!!AA SEQUENCE 1.0  
 ID AAB06485 standard; peptide; 10 AA.  
 AC AAB06485;  
 DT 28-SEP-2000 (first entry)  
 DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 492.  
 DE Claudin-1 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.  
 XX Mammalia.  
 OS Mammalia.  
 PN WO200026360-A1.  
 XX 11-MAY-2000.  
 XX 03-NOV-1999; 99WO-CA01029.  
 XX 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX Blaschuck OW, Symonds JM, Gour BJ;  
 WPI; 2000-365610/31.  
 XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 XX Claim 43; Page 96; 121pp; English.  
 XX The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.  
 XX Sequence 10 AA;  
 SQ

AAB06485 Length: 10 January 12, 2004 11:04 Type: P Check: 4174 ..

1 CWRIYSYAGC

!!AA SEQUENCE 1.0  
ID -AAB06491 standard; peptide; 10 AA.  
XX  
AC AAB06491;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 498.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06491 Length: 10 January 12, 2004 11:04 Type: P Check: 4192 ..  
1 KWR1YSYAGD

```

!!IAA SEQUENCE 1.0
ID AAB06497 standard; peptide; 10 AA.
XX
AC AAB06497;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 504.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06497 Length: 10 January 12, 2004 11:04 Type: P Check: 4202 ..

1 KWR1YSYAGE

!!AA\_SEQUENCE 1.0  
ID AAB06503 standard; peptide; 10 AA.  
XX AC AAB06503;  
XX DT 28-SEP-2000 (first entry)  
XX DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 510.  
XX KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX OS Mammalia.  
XX PN WO200026360-A1.  
XX PD 11-MAY-2000.  
XX PF 03-NOV-1999; 99WO-CA01029.  
XX PR 03-NOV-1998; 98US-0185908.  
XX PR 30-MAR-1999; 99US-0282029.  
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX PI Blaschuck OW, Symonds JM, Gour BJ;  
XX DR WPI; 2000-365610/31.  
XX PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX PS Claim 43; Page 97; 121pp; English.  
XX CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX SQ Sequence 10 AA;

AAB06503 Length: 10 January 12, 2004 11:04 Type: P Check: 4255 ..

1 DWRIYSYACK



!!IAA SEQUENCE 1.0  
 ID AAB06509 standard; peptide; 10 AA.  
 AC AAB06509;  
 XX 28-SEP-2000 (first entry)  
 XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 516.  
 DE Claudin-1 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.  
 XX Mammalia.  
 OS WO200026360-A1.  
 PN 11-MAY-2000.  
 XX 03-NOV-1999; 99WO-CA01029.  
 XX 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 PA Blaschuck OW, Symonds JM, Gour BJ;  
 PI WPI; 2000-365610/31.  
 DR Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 XX Claim 43; Page 97; 121pp; English.  
 XX The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.  
 XX Sequence 10 AA;  
 SQ

AAB06509 Length: 10 January 12, 2004 11:04 Type: P Check: 4256 ..

1 ENRIYSYACK

!!AA SEQUENCE 1.0  
ID -AAB06512 standard; peptide; 8 AA.  
AC AAB06512;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2000-365610/31.  
DR  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 97; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 8 AA;

AAB06512 Length: 8 January 12, 2004 11:04 Type: P Check: 2798 ..

1 WRIYSYAG

```

!!AA SEQUENCE 1.0
ID_AAB06521 standard; peptide; 8 AA.
XX
AC AAB06521;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 46; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

```

AAB06521 Length: 8 January 12, 2004 11:04 Type: P Check: 2954 ..

1 WRTSSYVG

!!AA SEQUENCE 1.0  
ID -AAB06530 standard; peptide; 10 AA.  
AC AAB06530;  
XX 28-SEP-2000 (first entry)  
XX  
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 119.  
XX  
XX Claudin-2 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
XX graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
XX WO200026360-A1.  
PN  
XX 11-MAY-2000.  
PD  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
PF  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR  
XX 30-MAR-1999; 99US-0282029.  
PR  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2000-365610/31.  
DR  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
PT  
XX  
PS Claim 49; Page 98; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
XX Sequence 10 AA;  
SQ  
AAB06530 Length: 10 January 12, 2004 10:59 Type: P Check: 4356 ..  
1 CWTSSYVGC

!!AA\_SEQUENCE 1.0  
ID AAB06539 standard; peptide; 10 AA.  
AC AAB06539;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 128.  
XX  
KW Claudin-2 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
XX graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 49; Page 98; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06539 Length: 10 January 12, 2004 10:59 Type: P Check: 4374 ..  
1 KWTSSYVGD

```

!!AA SEQUENCE 1.0
ID -AAB06548 standard; peptide; 10 AA.
XX
AC AAB06548;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 137.
XX
DE Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI; 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

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AAB06548 Length: 10 January 12, 2004 10:59 Type: P Check: 4384 ..

1 KWTSSYVGE

!!AA SEQUENCE 1.0  
ID -AAB06557 standard; peptide; 10 AA.  
XX  
AC AAB06557;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 146.  
XX  
KW Claudin-2 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 49; Page 98; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06557 Length: 10 January 12, 2004 11:00 Type: P Check: 4437 ..

1 DWTSSYVGK

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!!AA SEQUENCE 1.0
ID -AAB06566 standard; peptide; 10 AA.
XX
AC AAB06566;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 155.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 49; Page 98; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06566 Length: 10 January 12, 2004 11:00 Type: P Check: 4438 ..

1 EWTSSYVGK



```

!!AA SEQUENCE 1.0
ID AAB06574 standard; peptide; 8 AA.
AC AAB06574;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 49; Page 98; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

```

AAB06574 Length: 8 January 12, 2004 11:00 Type: P Check: 2954 ..

1 WRTSSYVG

!!AA SEQUENCE 1.0  
ID -AAB06583 standard; peptide; 8 AA.  
XX AC AAB06583;  
XX DT 28-SEP-2000 (first entry)  
XX DE Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.  
XX DE  
XX KW Claudin-3 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX OS Mammalia.  
XX PN WO200026360-A1.  
XX PD 11-MAY-2000.  
XX PF 03-NOV-1999; 99WO-CA01029.  
XX PR 03-NOV-1998; 98US-0185908.  
XX PR 30-MAR-1999; 99US-0282029.  
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX PI Blaschuck OW, Symonds JM, Gour BJ;  
XX DR WPI; 2000-365610/31.  
XX PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX PS Claim 52; Page 99; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX SQ Sequence 8 AA;

AAB06583 Length: 8 January 12, 2004 11:00 Type: P Check: 2665 ..

1 WRVSAFIG

```

!!AA SEQUENCE 1.0
ID -AAB06592 standard; peptide; 10 AA.
XX
AC AAB06592;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 225.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WC200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 99; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06592 Length: 10 January 12, 2004 11:00 Type: P Check: 4019 ..

1 CWRVSAFIGC

```

!!AA SEQUENCE 1.0
ID -AAB06601 standard; peptide; 10 AA.
XX
AC AAB06601;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 234.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO2000026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 99; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06601 Length: 10 January 12, 2004 11:00 Type: P Check: 4037 ..

1 KRVSAFIGD

```

!!AA SEQUENCE 1.0
ID -AAB06610 standard; peptide; 10 AA.
XX
AC AAB06610;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 243.
XX
DE Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PP 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 99; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;
AAB06610 Length: 10 January 12, 2004 11:00 Type: P Check: 4047 ..
1 KRVSAFIGE

```

!!AA SEQUENCE 1.0  
ID -AAB06619 standard; peptide; 10 AA.  
XX  
AC AAB06619;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 252.  
XX  
DE Claudin-3 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX  
XX WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 55; Page 100; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06619 Length: 10 January 12, 2004 11:00 Type: P Check: 4100 ..

```

!!AA_SEQUENCE 1.0
ID AAB06628 standard; peptide; 10 AA.
XX
AC AAB06628;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 261.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06628 Length: 10 January 12, 2004 11:01 Type: P Check: 4101 ..

1 EWRVSAFIGK

!!AA SEQUENCE 1.0  
ID AAB06636 standard; peptide; 8 AA.  
XX  
AC AAB06636;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 269.  
XX  
DE Claudin-3 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
XX graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 55; Page 100; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 8 AA;

AAB06636 Length: 8 January 12, 2004 11:01 Type: P Check: 2665 ..

1 WRVSAPIG



!!AA\_SEQUENCE 1.0  
ID AAB06645 standard; peptide; 8 AA.  
XX  
AC AAB06645;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
XX Claudin-4 cell adhesion recognition sequence SEQ ID NO: 50.  
XX  
XX Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
XX Mammalia.  
XX  
XX WO200026360-A1.  
PN  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
PF  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR  
XX 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX  
XX WPI; 2000-365610/31.  
DR  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
XX Claim 58; Page 100; 121pp; English.  
PS  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
XX  
SQ Sequence 8 AA;

AAB06645 Length: 8 January 12, 2004 11:01 Type: P Check: 2669 ..

1 WVRTAFIG

!!AA SEQUENCE 1.0  
ID -AAB06654 standard; peptide; 10 AA.  
XX  
AC AAB06654;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 172.  
XX  
DE Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
XX graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2000-365610/31.  
DR  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 61; Page 101; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06654 Length: 10 January 12, 2004 11:01 Type: P Check: 4024 ..  
1 CWRVTAFIGC

```

!!AA SEQUENCE 1.0
ID AAB06663 standard; peptide; 10 AA.
XX
AC AAB06663;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 181.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 61; Page 101; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;
AAB06663 Length: 10 January 12, 2004 11:01 Type: P Check: 4042 ..
1 KWRVTAFIGD

```

!!AA SEQUENCE 1.0  
ID AAB06672 standard; peptide; 10 AA.  
XX  
AC AAB06672;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 190.  
XX  
KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 61; Page 101; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06672 Length: 10 January 12, 2004 11:01 Type: P Check: 4052 ..

1 KWRVTAFIGE

!!AA SEQUENCE 1.0  
ID AAB06681 standard; peptide; 10 AA.  
XX  
AC AAB06681;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 199.  
XX  
KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 61; Page 101; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06681 Length: 10 January 12, 2004 11:01 Type: P Check: 4105 ..

1 DWRVTAFIGK

!!AA\_SEQUENCE 1.0  
ID AAB06690 standard; peptide; 10 AA.  
XX  
AC AAB06690;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 208.  
XX  
KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
XX graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 61; Page 101; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06690 Length: 10 January 12, 2004 11:02 Type: P Check: 4106 ..

1 EWRVTAFIGK

!!AA\_SEQUENCE 1.0  
ID AAB06698 standard; peptide; 8 AA.  
XX  
AC AAB06698;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 216.  
XX  
KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PP 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 61; Page 101; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 8 AA;

AAB06698 Length: 8 January 12, 2004 11:02 Type: P Check: 2669 ..

1 WRVTAFIG

```

!!AA SEQUENCE 1.0
ID -AAB06764 standard; peptide; 8 AA.
AC AAB06764;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1999; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 70; Page 103; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are adherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site.
XX
SQ Sequence 8 AA;

```

AAB06764 Length: 8 January 12, 2004 11:02 Type: P Check: 2655 ..

1 WKVTAFIG



```

!!AA SEQUENCE 1.0
ID -AAB06772 standard; peptide; 10 AA.
XX
AC AAB06772;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 343.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 103; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are adherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 10 AA;
AAB06772 Length: 10 January 12, 2004 10:57 Type: P Check: 4003 ..
1 CWKVTAFIGC

```

```

!!AA SEQUENCE 1.0
ID -AAB06781 standard; peptide; 10 AA.
XX
AC AAB06781;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 352.
XX
DE Claudin-6 modulating agent; claudin-9 modulating agent;
XX cell adhesion recognition sequence; CAR sequence; autoimmune disease;
XX inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 10 AA;

```

AAB06781 Length: 10 January 12, 2004 10:57 Type: P Check: 4021 ..

1 KWKVTAFIGD

```

!!AA SEQUENCE 1.0
ID AAB06789 standard; peptide; 10 AA.
XX
AC AAB06789;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 360.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are adherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 10 AA;

```

AAB06789 Length: 10 January 12, 2004 10:57 Type: P Check: 4031 ..

1 KWKVTAFIGE

!!AA SEQUENCE 1.0  
ID AAB06798 standard; peptide; 10 AA.  
XX  
AC AAB06798;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 369.  
XX  
KW Claudin-6 modulating agent; claudin-9 modulating agent;  
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
XX inflammatory disease; cancer; graft rejection; cyclic.  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 73; Page 104; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
CC are adherins, which are membrane glycoproteins involved in cell  
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
CC and these peptides can be used to modulate these levels, and thus treat  
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
CC healing and implant adhesion. In addition, they can also be used to  
CC facilitate drug delivery to the desired target site. The present  
CC sequence has a cyclic conformation.  
XX  
SQ Sequence 10 AA;  
AAB06798 Length: 10 January 12, 2004 10:57 Type: P Check: 4084 ..  
1 DWKVTAFIGK

```

!!AA_SEQUENCE 1.0
ID AAB06806 standard; peptide; 10 AA.
XX
AC AAB06806;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 377.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are adherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 10 AA;

```

AAB06806 Length: 10 January 12, 2004 10:59 Type: P Check: 4085 ..

1 EWKVTAFIGK

!!AA SEQUENCE 1.0  
ID -AAB06814 standard; peptide; 8 AA.  
XX  
AC AAB06814;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 385.  
XX  
KW Claudin-6 modulating agent; claudin-9 modulating agent;  
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
KW inflammatory disease; cancer; graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO2000026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 73; Page 104; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
CC are adherins, which are membrane glycoproteins involved in cell  
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
CC and these peptides can be used to modulate these levels, and thus treat  
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
CC healing and implant adhesion. In addition, they can also be used to  
CC facilitate drug delivery to the desired target site. The present  
CC sequence has a cyclic conformation.  
XX  
SQ Sequence 8 AA;

AAB06814 Length: 8 January 12, 2004 10:59 Type: P Check: 2655 ..

1 WKVTAFIG

!!AA SEQUENCE 1.0  
ID AAB06911 standard; Protein; 10 AA.  
XX  
AC AAB06911;  
XX  
DT 05-OCT-2000 (first entry)  
XX  
DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 475.  
XX  
DE Claudin modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "N-terminal acetyl or hydrogen"  
FT Modified-site 10 /note= "C-terminal amide"  
FT  
XX WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Disclosure; Page 19; 121pp; English.  
XX  
CC The present sequence is a peptide which can be used in a claudin-mediated  
CC cell adhesion modulator. The claudin group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and this peptide  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, it can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 10 AA;  
AAB06911 Length: 10 January 12, 2004 10:59 Type: P Check: 4176 ..  
1 WKIYSYAGDN

!!AA SEQUENCE 1.0  
ID AAB06916 standard; Protein; 8 AA.  
XX  
AC AAB06916;  
XX  
DT 05-OCT-2000 (first entry)  
XX  
DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 50.  
XX  
DE Claudin modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Synthetic.  
XX  
XX  
PH Key Location/Qualifiers  
FT Modified-site 1 /note= "N-terminal acetyl"  
FT Modified-site 8  
FT Modified-site 8 /note= "C-terminal amide"  
XX  
XX WO200026360-A1.  
XX  
XX 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2000-365610/31.  
DR  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
XX Claim 71; Page 103; 121pp; English.  
PS  
XX  
XX The present sequence is a peptide which can be used in a claudin-mediated  
CC cell adhesion modulator. The claudin group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and this peptide  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, it can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
XX Sequence 8 AA;  
SQ  
AAB06916 Length: 8 January 12, 2004 10:59 Type: P Check: 2655 ..  
1 WKYTAFIG



!!AA SEQUENCE 1.0  
ID AAB71661 standard; protein; 41 AA.  
XX  
AC AAB71661;  
XX  
DT 10-MAY-2001 (first entry)  
XX  
DE Human colon associated protein #9.  
XX  
KW Human; colon; cancer; disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200112781-A1.  
XX  
PD 22-FEB-2001.  
XX  
PF 11-AUG-2000; 2000MO-US22157.  
XX  
PR 13-AUG-1999; 99US-0148680.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Birse CE, Rosen CA;  
XX  
DR WPI; 2001-147551/15.  
XX  
PT Nucleic acids encoding 13 human colon cancer associated polypeptides,  
PT useful for preventing, diagnosing and/or treating e.g. cancers  
PT (especially colon cancer), Parkinson's disease and diabetic retinopathy  
PT -  
XX  
Claim 11; Page 320-321; 326pp; English.  
XX  
CC The present invention relates to 13 human colon cancer-associated  
CC proteins. These proteins and the nucleic acid encoding them may be  
CC used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate colon cancer-associated protein  
CC expression.  
XX  
SQ Sequence 41 AA;  
AAB71661 Length: 41 January 12, 2004 10:54 Type: P Check: 6573 ..  
1 MTGAGLGRDS GRWREVSFFG ETERARGGTV GRGRLRRQ E

!!AA SEQUENCE 1.0  
ID -AAU43488 standard; Protein: 50 AA.  
XX AC AAU43488;  
XX DT 27-FEB-2002 (first entry)  
XX DE Propionibacterium acnes immunogenic protein #4384.  
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
XX KW dermatological; osteopathic; neuroprotectant.  
XX OS Propionibacterium acnes.  
XX PN WO200181581-A2.  
XX PD 01-NOV-2001.  
XX PF 20-APR-2001; 2001WO-US12865.  
XX PR 21-APR-2000; 2000US-199047P.  
XX PR 02-JUN-2000; 2000US-208841P.  
XX PR 07-JUL-2000; 2000US-216747P.  
XX PA (CORI-) CORIXA CORP.  
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
XX DR WPI; 2001-616774/71.  
XX DR N-PSDB; AAS59520.  
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for  
XX PT vaccinating against and diagnosing infections, especially useful for  
XX PT treating acne vulgaris -  
XX PS Example 1; SEQ ID No 4683; 1069pp; English.  
XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
XX CC polypeptides. The proteins and their associated DNA sequences are used in  
XX CC the treatment, prevention and diagnosis of medical conditions caused by  
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
XX CC P. acnes is also involved in infections of bone, joints and the central  
XX CC nervous system, however it is particularly involved in the inflammatory  
XX CC lesions associated with acne vulgaris. A method for detecting the  
XX CC presence or absence of P. acnes in a patient comprises contacting a  
XX CC sample with a binding agent that binds to the proteins of the invention  
XX CC and determining the amount of bound protein in the sample. The  
XX CC polypeptides may be used as antigens in the production of antibodies  
XX CC specific for P. acnes proteins. These antibodies can be used to  
XX CC downregulate expression and activity of P. acnes polypeptides and  
XX CC therefore treat P. acnes infections. The antibodies may also be used as  
XX CC diagnostic agents for determining P. acnes presence, for example, by  
XX CC enzyme linked immunosorbent assay (ELISA).  
XX CC Note: The sequence data for this patent did not form part of the printed  
XX CC specification, but was obtained in electronic format directly from WIPO  
XX CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 50 AA;  
AAU43488 Length: 50 January 12, 2004 10:56 Type: P Check: 1666 ..  
1 WRPGSSPWRP WAFRGSSTTR SSLRCLRTG QSCFPSSVQR WLSLRMARSS

!!AA SEQUENCE 1.0  
ID ABB56595 standard; Peptide; 14 AA.  
XX AC ABB56595;  
XX DT 05-MAR-2002 (first entry)  
XX DE Human SNP related amino acid sequence SEQ ID NO:1160.  
XX KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;  
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
KW autoimmune disease; inflammation; cancer; nervous system disease;  
KW infection; polymorphic protein.  
XX OS Homo sapiens.  
XX PN WO200138586-A2.  
XX PD 31-MAY-2001.  
XX PF 22-NOV-2000; 2000WO-US32311.  
XX PR 24-NOV-1999; 99US-0167383.  
XX PA (CURA-) CURAGEN CORP.  
XX PI Shimkets RA, Leach M;  
XX DR WPI; 2001-355949/37.  
XX PT Isolated human nucleic acids comprising one or more single nucleotide  
PT polymorphisms, useful for treating a subject suffering from a  
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a  
PT sequence polymorphism -  
XX Claim 1; Page 599; 674pp; English.  
XX PS ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
CC to ABB56903 represent human peptides encoded by some of the SNP  
CC oligonucleotides. The sequences from the present invention can have  
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and  
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
CC and antibodies from the present invention can be used for treating a  
CC subject suffering from, at risk for, or suspected of, suffering from a  
CC pathology ascribed to the presence of a sequence polymorphism. The  
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
CC are also useful for determining which forms of a characterised  
CC polymorphism are present in individuals. The antibodies may be used in  
CC the detection, quantitation and/or cellular or tissue localisation of a  
CC polymorphic protein (e.g., for use in measuring levels of the  
CC polymorphic protein within appropriate physiological samples).  
XX SQ Sequence 14 AA;

ABB56595 Length: 14 January 12, 2004 10:55 Type: P Check: 8381 ..

1 MLLPSMRTSS YVGA

```

!!AA SEQUENCE 1.0
ID -ABB81045 standard; peptide; 8 AA.
XX
AC ABB81045;
XX
DT 05-NOV-2002 (first entry)
XX
DE Fab fragment directed against claudin CAR sequence.
XX
KW JAM; CAR; junctional adhesion molecule; cell adhesion; drug delivery;
KW angiogenesis; tumour; graft; transplant; wound; claudin.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8
FT /note= "C-terminal amide"
XX
PN US6391855-B1.
XX
PD 21-MAY-2002.
XX
PF 02-JUN-1999; 99US-0324541.
XX
PR 02-JUN-1999; 99US-0324541.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Symonds JM, Gour BJ;
XX
DR WPI; 2002-546108/58.
XX
PT Modulating agents for enhancing or inhibiting the action of junctional
PT adhesion molecule-mediated cell adhesion, useful in drug delivery,
PT anti-cancer treatment and wound repair -
XX
PS Disclosure; Column 32; 26pp; English.
XX
CC The invention provides modulating agents for enhancing or inhibiting the
CC action of junctional adhesion molecule (JAM)-mediated cell adhesion. The
CC cell adhesion modulating agent comprises : (a) at least five consecutive
CC amino acids of a JAM cell adhesion recognition (CAR) sequence as shown in
CC ABB81035 and (b) no more than 50 consecutive amino acid residues linked
CC by peptide bonds. The agents are useful in a wide variety of applications
CC including enhanced transdermal drug delivery, inhibition of angiogenesis,
CC inhibition of cell adhesion in tumours, increased healing of grafts,
CC transplants and wounds and in assessing the efficacy of other modulating
CC agents for JAM. The present sequence represents a Fab fragment directed
CC against claudin CAR sequence.
XX
SQ Sequence 8 AA;

```

ABB81045 Length: 8 January 12, 2004 10:57 Type: P Check: 2784 ..

1 WKIYSYAG

!!AA SEQUENCE 1.0  
ID ABP53938 standard; peptide; 9 AA.  
XX  
AC ABP53938;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:41.  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:41.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis;  
KW haemangioma; diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
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PF 16-JAN-2002; 2002WO-IB00099.  
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PR 17-JAN-2001; 2001US-262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
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PI Alitalo K, Koivunen E, Kubo H;  
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DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3  
PT activity, such as cancer and diseases of neovascularization -  
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PS Claim 14; Page 80; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to  
CC and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3).  
CC (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity  
CC of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle,  
CC ovary, skin, head and neck, oesophagus, bone, marrow or blood, and  
CC diseases of neovascularisation, e.g. liver diseases, hypertension,  
CC post-trauma, chronic hepatitis, haemangiomas and diabetes. The present  
CC sequence represents a specifically claimed VEGFR-3 binding peptide from  
CC the present invention.  
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SQ Sequence 9 AA;

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